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Morphological and physiological traits associated with barrenness and grain yield in the maize breeding population, Iowa Upright Leaf Synthetic #1

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INTRODUCTION

One of the major factors limiting optimum conversion of light energy into grain in maize (Zea mays L.) grown at high plant densities is barrenness, the failure of plants to produce seed-bearing ears. Grain yields of many contemporary hybrids and breeding populations planted at high densities are markedly reduced by this phenomenon. It is important, therefore, that factors influencing barrenness be determined, evaluated and understood so successful selection of genotypes that are tolerant to high plant densities can be accomplished.

Buren (1970) and Buren et al. (1974) identified various morphological and physiological plant traits associated with barrenness and grain yield of maize at high plant densities, and they proposed that genotypes possessing these traits should display reduced barrenness. Once maize breeding populations composed of genotypes possessing these traits have been produced, they should be amenable to yield improvement when planted at thick densities; and the probability of isolating high-yielding, density-tolerant genotypes from these populations should be enhanced.

Development of density-tolerant maize genotypes via incorporation of various morphological and physiological traits assumes the traits can be combined through breeding into one plant type. To determine whether or not these traits can be used in a breeding program, estimates of genetic variability, genetic correlations and heritabilities for them are needed.

Morphological and physiological traits are not commonly evaluated in maize breeding programs and, therefore, estimates of genetic variability and heritabilities are not available in the literature. Consequently, my research was conducted to:

1) determine magnitudes of genetic variability and heritabilities for various morphological and physiological traits of BSUL1,
2) determine which traits are associated with barrenness and grain yield at high plant densities,
3) develop selection indices (composed of the most important traits) upon which selection for yield potential can be based, and
4) estimate amounts of progress from selection for these traits in BSUL1.

LITERATURE REVIEW

Grain production of maize in the United States usually exceeds the combined totals of wheat, oats, soybeans, barley and rye. Use of improved hybrids, increased fertilizer-nitrogen rates and thick plant densities contributed greatly to an annual maize grain-yield increase of 1.57 q/ha during the past 20 years in the United States Corn Belt (Jugenheimer, 1976). In Iowa during the period 1960-1973, this increase was 1.9 q/ha/yr (Russell, 1974). Development of maize hybrids with resistance to diseases and lodging, more ears per plant and better adaptation to high plant densities and heavy fertilizer rates, therefore, is a prime objective of maize breeders interested in improving grain yield.

Barrenness, the failure of a plant to produce a normal ear, is a major factor that determines the optimum plant density for maize. However, barrenness also may be caused by damage from insects and diseases, and by unfavorable moisture availability and mineral nutrition at low plant densities (Buren, 1970). Optimum plant density for maize, therefore, is dictated by tolerance of maize genotypes to high densities and the availability of environmental resources to individual maize plants in the crop community (Termunde et al., 1963). Barrenness often is used as a criterion for classifying genotypes as either density tolerant or intolerant because high negative correlations between grain yield and barrenness at high plant densities have been well documented in the literature (Lang et al., 1956; Stinson and Moss, 1960; Pendleton and

Seif, 1961; Woolley et al., 1962; Stickler, 1964; Timmons et al., 1966; Rutger and Crowder, 1967; Buren, 1970). In three experiments reported by Buren et al. in 1974, correlation coefficients between grain yield and barrenness at 98,800 plants/ha ranged from -0.76 to -0.89.

Stinson and Moss (1960) suggested that competition for light is a principal cause of the inability of maize hybrids to tolerate dense plantings. They reported an average reduction in grain yield of 41 and 19% for intolerant and tolerant hybrids, respectively, when each was subjected to a 20% reduction in net radiation. Stinson and Moss (1960) concluded that maize hybrids differ in their capacity to utilize light in the production of grain and these differences are related to their level of performance in dense plantings. According to Prine (1961) and Prine and Schroder (1964), barrenness is due to mutual shading of leaves in the lower parts of the maize canopy. Evidence presented by Duncan (1958), Earley et al. (1967) and Pendleton et al. (1968) also indicated that light was a major factor limiting maize grain yields at high plant densities.

Mock and Pearce (1975) stated that the primary reason for increasing plant densities and narrowing row spacings for maize is the maximization of light interception and use. Saeki (1960), Monteith (1965) and Duncan (1969) suggested increasing leaf area per unit area of land (i.e., LAI) to maximize light interception and minimize amounts of light reaching the soil surface. To intercept and utilize light energy most efficiently, however, incident light must be distributed over a maximum amount of leaf area. Consequently, orientation of the maize canopy must be considered if one is to minimize mutual shading of lower leaves and permit distribution of light energy over the available leaf area.

Theoretically, plants with erectophile canopies should utilize light more efficiently than plants with planophile canopies when grown at high plant densities; however, plants with planophile canopies should be more efficient at low plant densities (Monteith, 1969). Loomis et al. (1968) reported that light penetration into maize canopies is largely determined by the orientation of the upper leaves, and Loomis et al. (1968) and Pendleton et al. (1968) hypothesized that maize varieties with erectophile upper canopies and planophile lower canopies should produce high grain yields at high plant densities. Results obtained by several researchers working with theoretical models (Duncan et al., 1967; Anderson and Denmead, 1969; Monteith, 1969; Duncan, 1971) have corroborated this hypothesis.

Associations of high grain yields and erect canopy-orientation have been reported in the literature. Pendleton et al. (1968) reported that a maize hybrid (Hy x C103) isogenic for the liguless (lg_2) gene for erect leaves displayed a 40% grain-yield increase relative to its normal counterpart when both were grown in 51-cm rows at 59,304 plants/ha. Additionally, Pendleton et al. (1968) manipulated the upper leaves of a commercial maize hybrid into an erect orientation and observed a 14.2% increase in grain yield compared to the same hybrid with its normal (horizontal) leaf orientation. Yield advantages of maize genotypes with erect leaves grown at high plant densities also have been demonstrated by Hopper (1970), Winter and Ohlrogge (1973), Pepper (1974), Fakorede (1975) and Mulamba (1977). Additionally, the maize ideotype proposed by Mock and Pearce

(1975) was characterized by stiff, vertically oriented leaves above the ear and horizontally oriented leaves below the ear.

Some studies have failed to demonstrate a grain-yield advantage for maize genotypes with erect canopies. Russell (1972) and Hicks and Stucker (1972) reported a negative grain-yield response to increased plant densities by erect-leaved maize hybrids. Furthermore, Duvick and Noble (1969) and Ariyanayagam et al. (1974) observed that erect-leaved maize genotypes were inconsistent in their yielding ability and, therefore, did not demonstrate a definite grain yield advantage over horizontal-leaved maize genotypes. Whigham and Woolley (1974) reported that erect-leaved genotypes produced slightly more total dry matter at high plant densities, but this advantage was not observed for grain yields.

Lonnquist and Jugenheimer (1943) and Sass and Loeffel (1959) suggested that the primary cause of barrenness is the lengthening of the anthesis-to-silking period, i.e., by the time late silks emerge, the pollen is not viable. The interval between anthesis and silking lengthens as plant density is increased (Kiesselbach, 1950; Dungan et al. 1958; Shaw and Thom, 1951; Woolley et al. 1962; Cardwell, 1967; Meyer, 1970; Buren, 1970; Fakorede, 1977). Additionally, Kohnke and Miles (1951) reported that silking was delayed approximately one day for every increase of 7,000 - 8,000 plants/ha. Maize hybrids intolerant of high plant densities have a longer delay in silk emergence than those that are tolerant (Moss and Stinson, 1961; Schwanke, 1965; Earley et al., 1967; Meyer, 1970; Buren, 1970; El-Lakany and Russell, 1971; Mock and Buren, 1972; Buren et al., (1974); Fakorede, 1977).

Traits associated with the maize flower often are correlated with barrenness and grain yield at high plant densities. Buren et al. (1974) reported that density-tolerant maize genotypes were characterized by rapid completion of silk extrusion, coincidence of pollen-shed and silk extrusion and rapid growth of the first ear and first-ear silk. Fakorede (1977) found that improved variety hybrids from advanced cycles of two recurrent selection programs exhibited earlier silking dates and reduced pollen-shed-to-silking intervals.

In an effort to determine the importance of pollen-shed-to-silking interval in the presence of adequate pollen supplies, Earley et al. (1966) hand-pollinated all plants with viable pollen; nevertheless, they observed a high degree of barrenness in some hybrids. These authors suggested, that since viable pollen was available, an extended pollen-shed-to-silking interval may not be the primary cause of barrenness. Moss and Stinson (1961) hypothesized, that since slow silk emergence and limited silk development were related, both of these phenomena were the manifestation of a more basic process. They suggested that hybrid differences in density tolerance were caused by differences in the translocation patterns of the photosynthate produced by the plants.

There is considerable evidence indicating density tolerance is related to an intra-plant competition (particularly between the developing tassel and ear primordia) for photosynthate. Leonard and Kiesselbach (1932), Grogan (1956), Duvick (1958) and Schwanke (1965) observed decreased barrenness and increased grain yields of detasselled maize plants when compared with grain yields of nondetasselled plants at high plant densities. Grogan (1956), suggested this phenomenon primarily was due to decreased competition for nutrients between the tassel primordia and ear primordia. Additionally, Duncan et al. (1967) and Hunter et al. (1969) hypothesized that positive yield responses associated with detasselling resulted from reduction of shading of upper canopy layers of maize plants grown at high densities. Duvick (1958) and Chinwuba et al. (1961) demonstrated significant decreases in barrenness and concomitant significant increases in grain yield at high plant densities when male-sterile hybrids were compared with their male-fertile counterparts. Chinwuba et al. (1961) harvested 41% more grain from male-sterile than from male-fertile hybrids at 68,000 plants/ha and concluded this was a consequence of reduced competition between the tassel and the ear. These conclusions were supported by the work of Sanford et al. (1965) which demonstrated that, at high plant densities, male-sterile plants displayed more nitrogen in the ear than in the tassel compared with male-fertile plants.

Mock and Buren (1972) and Buren et al. (1974) indicated that density-tolerant maize genotypes were characterized by, among other traits, small tassels. These authors mentioned that large tassels suppressed ear development of plants grown at high plant densities; and according to Anderson (1971), these repressive effects were probably caused by apical dominance created by increased auxin levels in the stem. Fakorede (1977) reported that maize variety hybrids from recurrent selection programs for grain yield displayed smaller tassels than their unimproved counterparts. Mock and Schuetz (1974) found tassel branch number was highly heritable, and they suggested that progress from selection for low tassel branch number and short tassel heights should be possible. Small tassels should reduce both the competitive ability of the tassel and shading of the upper leaves, and tassel size is a trait that should be considered in developing the maize ideotype suggested by Mock and Pearce in 1975.

Many workers have shown that prolific hybrids of maize show smaller genotype x environment interactions than one-eared hybrids and display less barrenness when planted at high plant densities (Freeman, 1955; Lang et al., 1956; Zuber and Grogan, 1956; Josephson, 1957; Bauman, 1960; Zuber et al., 1960; Collins et al., 1965; Andrew, 1967; Russell, 1968; Russell and Eberhart, 1968). Collins et al. (1965) compared 36 single crosses involving one-eared and two-eared inbred lines in an experiment grown two years at two locations with four plant densities at each location. The two-eared x two-eared single crosses were more stable in yield response to changes in densities and environments than the other hybrids. Collins et al. (1965) speculated that the presence of a second "outlet" for grain production may permit maximum utilization of available photosynthate. Work by Andrew (1967) showed barrenness was directly proportional to plant density, and single-eared maize hybrids showed more barrenness at the high density than multiple-eared hybrids. Russell (1968) found that single-eared genotypes grown at 29,000 pl/ha produced no second ears and had 11.9% barren plants at 58,100 pl/ha. Prolific genotypes, however, had 27% of the plants with second ears at 29,000 pl/ha, and they displayed only 3.0% barrenness at 58,100 pl/ha. Buren et al. (1974) reported that vigorous development of first and second ears of maize plants was negatively correlated with barrenness, suggesting that prolificacy should be a selection criterion used for breeding density-tolerant genotypes. Duvick (1974) increased prolificacy of maize inbred C103 through backcrossing and selection. When three "isogenic" selections of the prolific version were compared with the original C103 in hybrid combinations at three densities, the "prolifics" were significantly less barren and higher yielding than the original at the high density (i.e., 74,100 pl/ha). Furthermore, Russell and Prior (1975) showed that the variation for grain yield over a wide range of plant densities was much smaller for prolific maize hybrids than for nonprolific hybrids. Recently, Troyer and Brown (1976) observed that advanced cycles of seven maize synthetics adapted to Southern Iowa and grown in Southern Minnesota exhibited prolificacy at a low plant density after selection for reduced barrenness at high plant densities. Also, results from evaluations of long-term recurrent selection for increased yield of maize indicated that prolificacy had increased significantly (Fakorede, 1977; Moll and Kamprath, 1977).

Because grain yield is the ultimate product of the maize crop, the primary role of leaves on the maize plant is the production of carbohydrate through photosynthesis for storage in various organs during plant growth. Crosbie et al. (1977) studied CO_2 exchange rate (CER), an estimate of photosynthetic efficiency of 64 random inbred lines of maize derived from Iowa Stiff Stalk Synthetic (BSSS). They concluded that in BSSS one should realize substantial progress from selection for CER (i.e., 22% per cycle with a 15% selection intensity). Crosbie (1976) found, however, that genotypic correlations between CER and grain yield, grain-yield components, and total dry-matter yield were low. Consequently, selection for improved CER in BSSS would not increase the population's productivity. He hypothesized that grain yield was limited by either sink size, inefficient translocation of photosynthate to the ear or lack of a receptive sink. Recently, Fakorede (1977) reported that photosynthetic capacity was not limiting grain yield in BSSS, in Iowa Corn Borer Synthetic #1 (BSCB1) or in the variety 'Alph' (BS12). In his study, increased grain yields that resulted from recurrent selection were consequences of prolonged photosynthetic activity, increased production of photosynthate during grain filling and increased translocation of photosynthate from leaves to ears. Simmonds (1973) suggested that in cereals one yield-limiting factor may be inefficient transport of the photosynthate produced by the photosynthesizing tissues to the appropriate storage organs or sinks (i.e., grain). He further suggested that more photosynthate could be transported to the grain by reducing leafiness and overall plant size. Mock and Pearce (1975) emphasized that enhanced yield potential (i.e., photosynthetic efficiency) in a cereal such as maize is of little value unless the efficiency of conversion of photosynthate into grain is high.

Wallace et al. (1972) reported that leaf area was a major component contributing to economic yields and relative growth rates of crop plants. Grain production per unit leaf area, however, should be a better criterion for evaluating grain yield efficiency of maize genotypes (Earley, 1965). Mock and Buren (1972) and Buren et al. (1974) demonstrated that density-tolerant maize genotypes produced large amounts of grain per unit leaf area at high plant densities. Correlation coefficients for grain per unit leaf with grain yield and barrenness were 0.91 and -0.83, respectively (Buren et al., 1974). Additionally, Fakorede (1977) found that increased grain per unit leaf area was associated with selection for improved grain yield per se, and Mock and Pearce (1975) stressed the importance of grain per unit leaf area by characterizing their maize ideotype as a genotype that would utilize an optimum production environment by storing a maximum amount of photosynthate produced by the leaves in the grain.

Considerable data suggests plant-available moisture is a major factor causing reduced yields and increased barrenness of maize. Tatum (1954) reported that one type of drought damage is barrenness, and he observed one association between barrenness under droughty conditions and barrenness due to high plant densities. Research has shown that the most critical period for moisture stress, as well as other environmental stresses, includes the processes of pollen-shed, silking and fertilization. Lack of moisture during this period usually results in delayed silking and inadequate pollination and fertilization (Robins and Domingo, 1953; Zuber and Decker, 1956; Barnes and Woolley, 1969). Moisture stress during the tassel-emergence and silking period resulted in a 50% yield reduction compared to only a 20-25% yield loss for earlier or later periods of stress (Shaw and Loomis, 1950; Denmead and Shaw, 1960).

Increased barrenness resulting from increased plant density may be due to a lack of mineral nutrients. Lang et al. (1956) and Hinkle and Garrett (1961) reported that density stress was reduced at high levels of fertility; however, these authors concluded that barrenness was influenced more by plant density than by fertilizer-nitrogen levels. Similar results were obtained by Fakorede (1977).

Reports in the literature dealing with effects of planting date on barrenness corroborate the yield superiority associated with early dates. Cardwell (1967) observed that high-density-tolerant maize hybrids produced highest yields with early planting dates and lowest yields with late planting dates. Tolerant hybrids were affected less by date of planting than intolerant hybrids, but, they both exhibited decreased yield with delayed planting. Cardwell (1967) concluded that increased yields obtained with early planting dates were a function of reduced barrenness due to higher levels of sugar in the plant and higher nitrate-reductase activity. Several workers (Sayre et al., 1931; Van Reen and Singleton, 1952; Moss and Stinson, 1961; Sowell et al., 1961; Campbell, 1964) found sugar concentrations to be higher in barren plants than in plants bearing an ear, but no evidence indicates that hybrid differences in stalk-sugar content are causes of differential density tolerance.

Buren (1970) conducted an extensive literature review and concluded barrenness is a physiological response of the plant to inter-specific and intra-specific competition associated with stress due to insufficient mineral nutrition, low moisture, inadequate light and/or high plant densities. He suggested that barrenness could be reduced and density tolerance could be increased by selection.

Selection for improved yield potential and reduced barrenness often is accompanied by agronomically undesirable changes in some traits. High ear placement usually accompanies selection for high grain yield in maize (Josephson et al., 1976). Several long-term selection programs for yield resulted in increased prolificacy and harvest index but were accompanied by both increased plant and ear height, resulting in a greater susceptibility to lodging (Moll and Kamprath, 1977). Troyer and Brown (1976) reported that selecting for earlier flowering in unadapted maize synthetics increased yield but also resulted in an increase in the number of broken stalks.

Some evidence indicates that selection for improved density tolerance may be conducted at a low density. Buren (1970) found that days to silking, silking interval, anthesis-to-silking interval, dry weight of the top ear, dry weight of 100 seeds, number of second ears and tassel dry weight at anthesis all measured at a low plant density were the most important factors in the prediction equation for barrenness and grain yield at a high plant density. Subandi and Compton (1974) predicted that mass selection at a low plant density would improve the performance of the population at a high density. Furthermore, Troyer and Brown (1976) suggested that selection for prolificacy at a low stand level should result in reduced barrenness at a high plant density. Selection for improved yield of maize populations at 24,000 pl/ha resulted in average realized gains of 21 and 42% more yield than the original populations when grown at 38,300 and 49,420 pl/ha, respectively (Moll and Kamprath, 1977). Evidently, selection in maize for reduced barrenness and improved tolerance of high plant densities may be possible at low stand levels.

MATERIALS AND METHODS

Plant Materials and Management

My investigation was conducted in 1974, 1975 and 1976 at the Agronomy and Agricultural Engineering Research Center near Ames, Iowa. The breeding population used was Iowa Upright Leaf Synthetic #1 (BSUL1) which was synthesized by Dr. W. A. Russell from 16 inbred lines that exhibited erect leaf orientation (Table 1). Eight single-cross hybrids among pairs of the inbreds were made in 1969, and in the 1969-70 winter nursery, four double-cross hybrids were produced from the eight single crosses. In 1970, all possible hybrids were made among the four double crosses and progeny from these hybrids were random-mated in 1971 to produce the BSUL1 breeding population. Approximately 500 random plants from BSUL1 were self-pollinated in the 1973 breeding nursery, and the 288 plants with the best seed set were harvested to produce the S_1 lines for my study.

Cultural practices at the test sites were nearly identical each year. Nitrogen was applied before planting in the spring at a rate of 168 kg/ha, and 90 kg/ha P and K were applied in the autumns of 1973, 1974 and 1975. An additional 56 kg/ha N was sidedressed each year in mid-June. Weeds were controlled by application of a pre-plant herbicide (alachlor) at a rate of 3.2 ℓ/ha, by cultivation in early June and by hand weeding throughout the growing season.

Two-hundred-eighty-eight random S_1 lines from BSUL1 were planted in one-row plots (7 m long and spaced 102 cm apart) on April 27, 1974. The 288 lines were divided into two sets of 144 and were grown in two

Table 1. Parental lines of Iowa Upright Leaf Synthetic #1 (BSUL1)

Line	Derivation	Origin
B1	1159 - 1198	Iowa
B25	R4 - 66	Iowa
B52	-[a]	Iowa
B66	B33 x Oh43	Iowa
A257	Iowa Stiff Stalk Syn	Minnesota
Va43	Virginia Long Ear Syn	Virginia
H60	(MO21A x CI·14)(Oh28 x Oh51A)	Indiana
(Tux x Lanc(3 Syn) - 115	Tux x Lanc(3 Syn	Iowa
(Syn A) C1 - 112	(Syn A) C1	Iowa
Pa884P	K155 x A321	Pennsylvania
ITE701	Illinois Two Ear	Iowa
N28	Iowa Stiff Stalk Syn	Nebraska
(M14 x C103) - 1505	M14 x C103	Iowa
CBS#1 CY3C02	Iowa Corn Borer Syn #1	Iowa
HD2479	Iowa Stiff Stalk Syn	Iowa
(M14 x C103) - 1517	M14 x C103	Iowa

[a]Derivation unknown.

12 x 12 simple lattices with 2 replications. All rows were planted to a density of 101,600 pl/ha. The front 3 m of each row was thinned to 40,640 pl/ha (low density) but the back 4 m was not thinned (high density). Final stands in the high density usually ranged from 76,200 to 101,600 pl/ha. Because of heavy rains and temporary flooding in the field, however, stands in some plots were poor, resulting in reduced competition within and between plots.

Because seed supplies of many of the S_1 lines were limited, one-row plots were used in my 1974 experiment. Poor stands, however, resulted in unequal inter-row competition between some of the single-row plots, especially at the high density. Furthermore, plant heights and leaf orientations of the S_1 lines were drastically different. These observations suggested bordered plots should be used in subsequent experiments. Therefore, to obtain sufficient amounts of seed to permit planting of bordered plots, seed supplies from all 288 S_1 lines were increased by sib-mating 6 to 17 plants per line in the 1974 breeding nursery and bulking equal amounts of seed from each sib-mated plant within a line. Also, to reduce costs of conducting the experiment, only one set (i.e., 144) of the original 288 S_1 lines was evaluated in 1975 and 1976.

Seeds from 144 S_1 families of BSUL1 (increased in 1974) were planted in three-row plots (7 m long, with rows spaced 102 cm apart) on May 12, 1975 and May 5, 1976. The front 3 m of each row was over-planted and thinned to a density of 42,383 pl/ha and the back 4 m was over-planted and thinned to a density of 96,875 pl/ha. Experiments each year were arranged in 12 x 12 simple lattices with 2 replications. Data were collected only from plants in the center row of each plot.

Experimental Technique

S_1 families were evaluated for several morphological and physiological traits at each plant density. The traits measured each year and an explanation of the abbreviations used to identify these traits are presented in Table 2.

Canopy orientation traits

Leaf orientation values Measurements necessary to calculate leaf orientation values (LOV) were recorded on five plants per plot at each density. LOV's for the most recently expanded leaves of juvenile plants measured on July 1 (LOV_j) and for leaves above (LOV_a) and below (LOV_b) the ears of mature plants measured during grain filling were calculated by Pepper's (1974) formula:

$$LOV = \sum_{i=1}^{n} [\theta(\ell_f/\ell)]_i/n$$

where θ = leaf angle (degrees from horizontal) at point of attachment of leaf blade to plant stem

ℓ_f = length (cm) of leaf from collar to point where the blade became parallel to the soil surface (i.e., "flagged")

ℓ = total length (cm) of leaf

n = number of plants measured per plot (i.e., 5).

Table 2. Abbreviations used to identify the traits of random S_1 lines from BSUL1 and the densities at which these traits were measured in 1974, 1975 and 1976

Abbreviation	Description
Canopy Orientation	
LOV_j	Leaf orientation value of juvenile plants
LOV_a	Leaf orientation value of canopy above ear
LOV_b	Leaf orientation value of canopy below ear
LOR_j	Leaf orientation rating of juvenile plants
LOR_m	Leaf orientation rating of mature plants
Plant	
ERHT	Ear height (cm)
PTHT	Plant height (cm)
ERHT:PTHT	Ratio of ear height to plant height
PLA	Leaf area per plant (cm^2)
TBN	Tassel branch number
LODG	Lodged plants at harvest (%)
Flowering	
25%ANTH	Days from July 1 to 25% anthesis
50%ANTH	Days from July 1 to 50% anthesis
75%ANTH	Days from July 1 to 75% anthesis
25%SILK	Days from July 1 to 25% silk-emergence
50%SILK	Days from July 1 to 50% silk-emergence
75%SILK	Days from July 1 to 75% silk-emergence
PSS	Pollen-shed-to-silking interval (days)
SI	Silking interval (days)
SD	Silking delay (days)
Harvest	
YIELD	Grain yield per plot (q/ha)
YIELDP	Grain yield per plant (g)
BARREN	Barren plants (%)
PROLIF	Number of ears per 100 plants
SECOND	Second ear grain as a percentage of total grain weight
GRNPLA	Grain yield per unit leaf area (g/dm^2)
STAND	Plant stand at harvest
Photosynthetic Capacity	
CER	CO_2 exchange rate (mg $CO_2/dm^2/hr$)
SLW	Specific leaf weight (mg/cm^2)
LT	Leaf thickness (μ)

[1]Measured at above density.

1974		1975		1976	
plants per hectare		plants per hectare		plants per hectare	
101,600	40,640	96,875	42,383	96,875	42,383
	x	x	x		
	x	x	x	x	x
	x	x	x		
	x		x		x
	x		x		
	x	x	x	x	x
	x	x	x	x	x
	x	x	x	x	x
x[1]	x	x	x		
	x	x	x	x	x
		x	x	x	x
		x	x	x	x
x		x	x	x	x
		x	x	x	x
		x	x	x	x
x		x	x	x	x
		x	x	x	x
x		x	x	x	x
x		x	x	x	x
		x	x	x	x
x		x	x	x	x
		x	x	x	x
x		x	x	x	x
	x	x	x	x	x
			x		x
x	x	x	x	x	x
x	x	x	x	x	x
	x		x		x
	x		x		x
	x		x		x

Leaf orientation ratings   Leaf-orientation-rating (LOR) procedures were developed to permit rapid evaluation of canopy orientation. Juvenile leaf orientation ratings (LOR_j) were made on July 1 and were based on the following scale:

1 = leaves oriented less than 45^o from horizontal

2 = leaves oriented approximately 45^o from horizontal

3 = leaves oriented more than 45^o from horizontal.

Leaf orientation ratings for mature plants (LOR_m) were estimated during grain filling as follows:

1 = leaves oriented less than 45^o from horizontal

2 = leaves oriented approximately 45^o from horizontal

3 = all leaves oriented more than 45^o from horizontal

4 = leaves oriented more than 45^o from horizontal above the ear only, leaf blade became parallel to the soil surface (i.e., "flagged")

5 = leaves oriented more than 45^o from horizontal above the ear only, leaf blade did not become parallel to the soil surface (i.e., stiff).

LOR estimates for each plot were averages of two independent ratings.

Plant traits

Ear and plant heights   I measured ear and plant heights of mature plants as distances in cm from the soil surface to the point of primary ear attachment (ERHT) or to the collar of the flag leaf (PTHT), respectively. Additionally, ear-to-plant-height ratio (ERHT:PTHT) was calculated by dividing the ear height by the plant height of individual plants.

These measurements were recorded for five competitive plants per plot.

Leaf area I measured length (L_ℓ) and maximum width (L_w) of the eighth leaf below the tassel on five competitive plants during grain filling and calculated leaf area by the formula (Montgomery, 1911):

$$A = L_\ell \times L_w \times 0.75.$$

Leaf area per plant (PLA) was estimated by multiplying the area of leaf number eight by the leaf-area factor, 9.39, developed by Pearce, Mock and Bailey (1975).

Tassel branch number (TBN) After pollen shed, I recorded tassel branch number (including the central branch) for five competitive plants per plot.

Percent lodging (LODG) Immediately before harvest, I estimated combined stalk and root lodging for each plot. My counts of lodged plants included plants broken below the ear, plus plants inclined more than 30° from vertical. These counts were divided by the total number of plants per plot and expressed as percentages.

Flowering traits

Flowering dates Ten random plants were tagged in each density and the date when each tagged plant displayed silk extrusion and dehiscent anthers at least half-way down the central tassel branch (anthesis) was recorded as days from July 1. From these data, days from July 1 to 25%, 50%, 75% anthesis (ANTH) and days from July 1 to 25%, 50%, 75% silk emergence (SILK) were calculated.

Flowering duration   Three estimates of flowering duration were obtained. Pollen-shed-to-silking interval (PSS) is a measure of the coincidence of anthesis and silk emergence for a plot and was expressed in days (i.e., 50%SILK minus 50%ANTH). Silking interval (SI) is a measure of the uniformity of silking rate for each plot and was calculated as 75%SILK minus 25%SILK. Silking delay (SD) is an estimate of the coincidence of anthesis and silk emergence on an individual plant basis and was calculated as follows:

$$SD = \sum_{i=1}^{n} (SILK - ANTH)_i / n$$

where SILK = days from July 1 to silk emergence

ANTH = days from July 1 to anthesis

n = number of plants measured per plot (i.e., 10).

Harvest traits

Grain yield   My experiments were harvested beginning on October 10, 1974, October 15, 1975 and October 11, 1976. Ears were harvested from all plants (only in the center row of the three-row plots used in 1975 and 1976) excluding two hills at each end of the low density and three hills at each end of the high density. All ears were dried to a constant moisture and visually rated for percentage of cob covered with grain. Ears having less than 25% of their cobs covered with grain were considered barren and discarded. The remaining ears, counted as harvestable ears, were shelled and weighed. Grain yield per hectare (YIELD) was estimated by dividing the sample grain weight by the plot land area and converting to quintals per hectare (q/ha). Grain yield per plant (YIELDP) was estimated by dividing the sample grain weight by the number of plants harvested in each plot.

Barrenness   Plants that did not produce ears with at least 25% of their surfaces covered with kernels were considered to be barren. Percentage barrenness (BARREN) was estimated by dividing the number of barren plants by the total number of plants in the plot and multiplying by 100.

Prolificacy   Number of ears per 100 plants (PROLIF) was estimated by dividing the number of harvestable ears by the total number of plants per plot and multiplying by 100. I used yield of second-ear grain as an additional estimate of prolificacy. Second ears were shelled, their grain weighed separately and these weights were expressed as percentages of the total yield per plot (SECOND).

Grain per leaf area   Grain yield per unit plant leaf area (GRNPLA) was estimated by dividing the weight of grain produced per plant by the estimate of leaf area per plant and was expressed as g/dm^2. Because of severe leaf shredding caused by a hailstorm on June 30, 1976, some measurements of canopy orientation (LOV_j, LOV_b, LOR_j) and leaf area per plant (PLA) were not made. Consequently, no estimation of GRNPLA was made in the 1976 experiment.

Photosynthetic capacity

To estimate photosynthetic capacity of BSUL1, a random sample of 64 of the 144 S_1 families was evaluated for CO_2 exchange rate (CER) during grain filling by the detached-leaf-leaf-section method described by Pearce, Crosbie and Mock (1976). This experiment was sampled as an 8 x 8 simple lattice beginning August 26, 1974, August 11, 1975 and August 16, 1976. All measurements were made on the second leaf below the tassel of four randomly chosen plants in the low density only, and plot means were calculated from individual plant data. These measurements were made on plants in the center row of the three-row plots used in 1975 and 1976. Estimates of specific leaf weight (SLW) and leaf thickness (LT) also were obtained from the same four plants used to measure CER according to the procedures described by Crosbie (1976). The 64 random lines sampled in 1974 were from a different set of 144 S_1 lines than those sampled in 1975 and 1976.

Statistical Analyses

Analyses of variance and covariance

Analyses of variance for all traits at each density were based on the following linear model for a lattice design:

$$Y_{ijk} = m + R_i + B_{ij} + G_k + e_{ijk}$$

where Y_{ijk} = observed value for the ijk^{th} plot

m = the overall experiment mean

R_i = effect of the i^{th} replication, $i = 1, 2$

B_{ij} = effect of the j^{th} incomplete block within the i^{th} replication, $j = 1, 2, \cdots, 12$

G_k = effect of the k^{th} genotype, $k = 1, 2, \cdots, 144$

e_{ijk} = random error.

Components for these analyses of variance (Cochran and Cox, 1957) are shown in Table 3.

In 1974, two sets of 144 random S_1 lines were evaluated and an analysis of variance was pooled over sets as outlined in Table 4.

Data for each trait from the 1975 and 1976 experiments were combined over environments (years) and analyzed using adjusted means. The linear model for these analyses was:

$$Y_{i\ell} = m + E_i + G_\ell + (GE)_{i\ell}$$

where $Y_{i\ell}$ = adjusted mean of the ℓ^{th} genotype in the i^{th} environment

m = overall mean

E_i = effect of the i^{th} environment, $i = 1, 2$

G_ℓ = effect of the ℓ^{th} genotype, $\ell = 1, 2, \cdots, 144$

$(GE)_{i\ell}$ = effect of the genotype x environment interaction.

The combined analysis of variance associated with this model is shown in Table 5. Estimates of σ_e^2 were obtained by pooling effective error sums of squares from both environments. Similarly, sums of squares for replications were obtained by pooling replication sums of squares from each environment.

Components of variance for traits measured in one environment were estimated from the expected mean squares presented in Table 3 as follows:

$$\hat{\sigma}_e^2 = M_1$$

Table 3. Components of analysis of variance for one plant density

Source		df	MS	E(MS)
Replications	$(r-1)$	1		
Genotypes	(k^2-1)	143	M_2	$\sigma_e^2 + r\sigma_G^2$
Unadjusted				
Adjusted				
Blocks/reps	$r(k-1)$	22		
Error				
Randomized block	$(r-1)(k^2-1)$	143		
Intra-block	$(k-1)(rk-k-1)$	121		
Effective	$(k-1)(rk-k-1)$	121	M_1	σ_e^2
Total	(rk^2-1)	287		

Table 4. Components of analysis of variance pooled over sets of lines

Source		df	MS	E(MS)
Sets	(s-1)	1		
Reps/sets	s(r-1)	2		
Genotypes/sets	$s(k^2-1)$	286	M_2	$\sigma_e^2 + r\sigma_G^2$
Unadjusted				
Adjusted				
Blocks/sets	sr(k-1)	44		
Pooled error				
Randomized block	$s(r-1)(k^2-1)$	286		
Intra-block	s(k-1)(rk-k-1)	242		
Effective	s(k-1)(rk-k-1)	242	M_1	σ_e^2
Total	(srk^2-1)	575		

Table 5. Components of analysis of variance combined over environments

Source		df	MS	E(MS)
Environments (E)	(e-1)	1	M_5	
Replications/E	e(r-1)	2	M_4	
Genotypes (G)	(k^2-1)	143	M_3	$\sigma_e^2 + r\sigma_{GE}^2 + re\sigma_G^2$
G x E	$(k^2-1)(e-1)$	143	M_2	$\sigma_e^2 + r\sigma_{GE}^2$
Pooled effective error	e[(k-1)(rk-k-1)]	242	M_1	σ_e^2
Total	(erk^2-1)	575		

$$\hat{\sigma}^2_{ph} = \frac{M_2}{r}$$

$$\hat{\sigma}^2_{G} = \frac{M_2 - M_1}{r} .$$

The variance of $\hat{\sigma}^2_G$ was calculated as outlined by Comstock and Moll (1963).

$$V(\hat{\sigma}^2_G) = \frac{1}{r^2} \left[\frac{2(M_2)^2}{(k^2 - 1) + 2} + \frac{2(M_1)^2}{(k - 1)(rk - k - 1) + 2} \right]$$

where k = the number of treatments per block (i.e., 12).

Estimates of variance components were obtained from expected mean squares from the combined analysis of variance (Table 5) as follows:

$$\hat{\sigma}^2_e = M_1$$

$$\hat{\sigma}^2_{ph} = \frac{M_3}{re}$$

$$\hat{\sigma}^2_{GE} = \frac{M_2 - M_1}{r}$$

$$\hat{\sigma}^2_G = \frac{M_3 - M_2}{re} .$$

Variances for these components also were computed using formulas of Comstock and Moll (1963).

$$V(\hat{\sigma}^2_{GE}) = \frac{1}{r^2} \left[\frac{2(M_2)^2}{(k^2 - 1)(e - 1) + 2} + \frac{2(M_1)^2}{e[(k - 1)(rk - k - 1) + 2]} \right]$$

$$V(\hat{\sigma}^2_G) = \frac{1}{(re)^2} \left[\frac{2(M_3)^2}{(k^2 - 1) + 2} + \frac{2(M_2)^2}{(k^2 - 1)(e - 1) + 2} \right]$$

The combined analysis of covariance is shown in Table 6. Components of covariance were calculated as:

$$\hat{\sigma}_{e_{xy}} = M_{1_x} M_{1_y}$$

$$\hat{\sigma}_{G_{xy}} = \frac{M_{3_x} M_{3_y} - M_{2_x} M_{2_y}}{re} .$$

Estimates of heritability

I estimated broad-sense heritabilities on an entry-mean basis in one environment by the formula:

$$h^2 = \frac{\hat{\sigma}^2_G}{\frac{\hat{\sigma}^2_e}{r} + \hat{\sigma}^2_G}$$

where $\hat{\sigma}^2_G$ = estimated genotypic variance

$\hat{\sigma}^2_e$ = estimated error variance

r = number of replications (i.e., 2).

Similarly, variance components from the combined analyses of variance were used to compute broad-sense heritability estimates on an entry-mean basis as follows:

$$h^2 = \frac{\hat{\sigma}^2_G}{\frac{\hat{\sigma}^2_e}{re} + \frac{\hat{\sigma}^2_{GE}}{e} + \hat{\sigma}^2_G}$$

where $\hat{\sigma}^2_G$ = estimated genotypic variance

Table 6. Components of analysis of covariance for traits x and y combined over environments

Source		df	Mean cross product	Expected mean cross product
Environments (E)	(e-1)	1	$M_{5_x} M_{5_y}$	
Replications/E	e(r-1)	2	$M_{4_x} M_{4_y}$	
Genotypes (G)	(k^2-1)	143	$M_{3_x} M_{3_y}$	$\sigma_{e_{xy}} + r\sigma_{GE_{xy}} + re\sigma_{G_{xy}}$
G x E	$(k^2-1)(e-1)$	143	$M_{2_x} M_{2_y}$	$\sigma_{e_{xy}} + r\sigma_{GE_{xy}}$
Error	$e(k^2-1)(r-1)$	242	$M_{1_x} M_{1_y}$	$\sigma_{e_{xy}}$
Total	(erk^2-1)	575		

$\hat{\sigma}^2_{GE}$ = estimated genotype x environment interaction variance

$\hat{\sigma}^2_e$ = estimated error variance

e = number of environments (i.e., 2)

r = number of replications (i.e., 2).

I calculated standard errors for these estimates according to the procedures outlined by Pesek and Baker (1971).

Phenotypic, genotypic and error correlations

I computed phenotypic correlations between all pairs of traits by the formula:

$$r_{ph_{xy}} = \frac{M_{3_x}M_{3_y}}{\sqrt{M_{3_x} \cdot M_{3_y}}}$$

where $r_{ph_{xy}}$ = phenotypic correlation coefficient for traits x and y

$M_{3_x}M_{3_y}$ = genotype mean cross product for traits x and y

M_{3_x} = genotype mean square for trait x

M_{3_y} = genotype mean square for trait y.

Components of variation and covariation (Tables 3, 4, 5 and 6) were used to estimate genotypic ($r_{g_{xy}}$) and error ($r_{e_{xy}}$) correlations for important pairs of traits (Mode and Robinson, 1959).

$$r_{g_{xy}} = \frac{\hat{\sigma}_{G_{xy}}}{\sqrt{\hat{\sigma}^2_{G_x} \cdot \hat{\sigma}^2_{G_y}}}$$

where $r_{g_{xy}}$ = genotypic correlation coefficient for traits x and y

$\hat{\sigma}_{G_{xy}}$ = genotypic covariance between traits x and y

$\hat{\sigma}^2_{G_x}$ = genotypic variance of trait x

$\hat{\sigma}^2_{G_y}$ = genotypic variance of trait y.

$$r_{e_{xy}} = \frac{\hat{\sigma}_{e_{xy}}}{\sqrt{\hat{\sigma}^2_{e_x} \cdot \hat{\sigma}^2_{e_y}}}$$

where $r_{e_{xy}}$ = error correlation coefficient for traits x and y

$\hat{\sigma}_{e_{xy}}$ = error covariance of traits x and y

$\hat{\sigma}^2_{e_x}$ = error variance of trait x

$\hat{\sigma}^2_{e_y}$ = error variance of trait y.

Multiple regression and factor analysis

Multiple regression models (Steel and Torrie, 1960) were fit using grain yield or barrenness as the dependent variable. This was done to examine the effectiveness of groups of traits for predicting the dependent variable at both plant densities and to estimate the relative importance of the traits in different models.

Stepwise multiple regression analysis (forward selection) was performed as outlined by Draper and Smith (1967). According to this method, the multiple regression equation and multiple coefficient of determination (R^2) were obtained by adding independent variables one at a time according to their relative importance in determining the dependent variable, grain yield or barrenness.

Factor analysis, described by Cattell (1965) and Morrison (1967), was performed in an attempt to group the traits on the basis of common causative influences. Basically, factor analysis expresses a single variable as a linear function of underlying factors. The linear model includes terms for m uncorrelated factors (acting on two or more variables) and a specific factor for each variable (Ottaviano et al., 1975). The factor model is represented as:

$$X_1 = a_{11}F_1 + a_{12}F_2 + \cdots\cdots + a_{1m}F_m + e_1$$

$$X_2 = a_{21}F_1 + a_{22}F_2 + \cdots\cdots + a_{2m}F_m + e_2$$

$$\vdots$$

$$X_p = a_{p1}F_1 + a_{p2}F_2 + \cdots\cdots + a_{pm}F_m + ep$$

which, in matrix notation, can be reduced to

$$X = \alpha f + e$$

where

X = vector of observed variables

α = matrix of the a_{ij} coefficients (factor loadings), $i = 1, \ldots, p$, $j = 1, \ldots m$

f = vector of factors

e = vector of specific components.

For computing factors, the matrix of correlations among variables was first reduced to represent only common variation; i.e., unities in the diagonal vector of the correlation matrix were replaced by communalities. Communality is the amount of variance of a variable accounted for by all factors collectively, and is the R^2 value obtained by regressing a variable on all other variables in the model (Lee and Kaltsikes, 1973; Eckert and Westfall, 1975; Ottaviano et al., 1975). Characteristic roots and vectors were obtained from the reduced correlation matrix. These were rotated by the varimax rotation method and the resulting rotated factors were orthogonal (Kaiser, 1958). The proposed application of factor analysis to maize breeding was outlined by Fakorede, Smith and Mock (1978).

Selection Procedures

Single-trait selection

Predicted advance from single-trait selection at each plant density was calculated by the formula (Allard, 1960):

$$\Delta G_i = k \cdot \hat{\sigma} ph_i \cdot h^2$$

where ΔG_i = predicted selection advance for the i^{th} trait

k = standardized selection differential

$\hat{\sigma}_{ph_i}$ = phenotypic standard deviation of the i^{th} trait

h^2 = heritability.

Correlated genetic responses in yield and barrenness when selection was directed exclusively to other traits was calculated by the formula (Johnson et al., 1955):

$$\Delta G_i = \frac{k\hat{\sigma}_{F_{yi}}}{\sqrt{\hat{\sigma}^2_{ph_y}}}$$

where ΔG_i = genetic response for the i^{th} trait

k = standardized selection differential

$\hat{\sigma}_{F_{yi}}$ = genotypic covariance between selected and i^{th} trait

$\hat{\sigma}^2_{ph_y}$ = phenotypic variance of selected trait.

Index selection

Procedures for construction of selection indices were described by Smith (1936) and Hanson and Johnson (1957). Let H be the aggregate genetic value of an individual, G_i the genotypic worth of a particular trait, and a_i the corresponding relative economic weight. Then, the genotypic value of the individual would be expressed as:

$$H = a_1G_1 + a_2G_2 + \cdots + a_nG_n = \Sigma_i a_i G_i.$$

The genotypic values cannot be directly evaluated since measurements are made on phenotypes which include nonheritable variations that do not accurately represent their genotypes. Therefore, an index, I, which is defined as a linear function of traits, is constructed so it has maximum correlation with the aggregate genetic value of the individual.

The index is of the form:

$$I = b_1X_1 + b_2X_2 + \cdots + b_nX_n = \Sigma_i b_i X_i$$

where the X_i's are observed phenotypic values of traits and the b_i's are weights to be given to the various traits considered in selection.

Letting the genotypic covariance of G_i and G_j equal G_{ij} (i, j = 1, $\cdots$, n) and the phenotypic covariance of X_i and X_j equal P_{ij}, then

$$V(H) = a_1^2G_{11} + a_2^2G_{22} + \cdots + 2a_1a_2G_{12} + \cdots = \Sigma_i\Sigma_j a_i a_j G_{ij}$$

$$V(I) = b_1^2P_{11} + b_2^2P_{22} + \cdots + 2b_1b_2P_{12} + \cdots = \Sigma_i\Sigma_j b_i P_{ij}$$

$$Cov(HI) = a_1b_1cov_{G_1X_1} + a_2b_2cov_{G_2X_2} + \cdots a_1b_2cov_{G_1X_2} + a_2b_1cov_{G_2X_1} + \cdots = \Sigma_i\Sigma_j a_i b_j G_{ij}.$$

The regression of H on I is obtained by the expression:

$$B_{HI} = \frac{Cov(HI)}{V(I)}$$

and

$$B_{HI}[V(I)]^{\frac{1}{2}} = \frac{Cov(HI)}{\sqrt{V(I)}}$$

then

$$\log B_{HI}[V(I)]^{\frac{1}{2}} = \log Cov(HI) - \tfrac{1}{2}\log V(I).$$

The values of the b's, which are the multiple regression coefficients, are computed to maximize the above equations. These values can be calculated from n simultaneous equations:

$$b_1P_{11} + b_2P_{12} + \cdots + b_nP_{1n} = a_1G_{11} + a_2G_{12} + \cdots + a_nG_{1n}$$

$$b_1P_{21} + b_2P_{22} + \cdots + b_nP_{2n} = a_1G_{21} + a_2G_{22} + \cdots + a_nG_{2n}$$

$$\vdots$$

$$b_1P_{n1} + b_2P_{n2} + \cdots + b_nP_{nn} = a_1G_{n1} + a_2G_{n2} + \cdots + a_nG_{nn}$$

or in general form, $\Sigma_j b_j P_{ij} = \Sigma_j a_j G_{ij}$

where i is constant in each equation. The solution of these equations for b_j is:

$$b_j = \Sigma_j a_j G_{ij} C_{ji}$$

where the values of C_{ji} are given by the matrix,

$$\begin{matrix} C_{11} & C_{21} & \cdots\cdots & C_{n1} \\ C_{12} & C_{22} & \cdots\cdots & C_{n2} \\ \vdots & \vdots & & \vdots \\ C_{1n} & C_{2n} & \cdots\cdots & C_{nn} \end{matrix}$$

which is the inverse of,

$$\begin{matrix} P_{11} & P_{21} & \cdots\cdots & P_{n1} \\ P_{12} & P_{22} & \cdots\cdots & P_{n2} \\ \vdots & \vdots & & \vdots \\ P_{1n} & P_{2n} & \cdots\cdots & P_{nn}. \end{matrix}$$

The change in H, aggregate genetic value, expected from truncation selection on I for any set of b_j's is:

$$H = kB_{HI}[V(I)]^{\frac{1}{2}} = k\frac{Cov(HI)}{\sqrt{V(I)}} = k\frac{\Sigma_i\Sigma_j b_j a_i G_{ij}}{\sqrt{\Sigma_i\Sigma_j b_i b_j P_{ij}}}\ .$$

Now, substituting for b_j in $V(I) = \Sigma_i\Sigma_j b_i b_j P_{ij}$

$$= \Sigma_i\Sigma_j b_i a_j G_{ij} C_{ji} P_{ij}$$

$$= \Sigma_i\Sigma_j b_i a_j G_{ij}$$

$$= Cov(HI).$$

The genetic change then reduces to:

$$\Delta H = k\sqrt{Cov(HI)}$$

$$= k\sqrt{\Sigma_i\Sigma_j b_j a_i G_{ij}}$$

where k is the selection differential in standard units.

The expected genetic changes for the individual traits involved in the index can be calculated using the regression of trait j on the index. The regression of trait j on I is:

$$B_{G_jI} = \frac{Cov(G_jI)}{V(I)} = \frac{\Sigma_i b_i G_{ij}}{\Sigma_i\Sigma_j b_j a_i G_{ij}}\ .$$

Then, the expected genetic change for the j^{th} trait (in the units of the trait) from selection on the basis of the index is found to be

$$\Delta G_j = kB_{G_jI}[V(I)]^{\frac{1}{2}}$$

$$= k \frac{Cov(G_j I)}{\sqrt{V(I)}}$$

$$= k \frac{\Sigma_i b_i G_{ij}}{\sqrt{\Sigma_i \Sigma_j b_j a_i G_{ij}}} .$$

These separate genetic changes when weighted with their relative economic values add up to the total genetic change:

$$\Delta H = a_1 \Delta G_1 + a_2 \Delta G_2 + \cdots + a_n \Delta G_n .$$

Similarly, the expected genetic changes for traits not involved in the index can be calculated using the regression of those traits on the index. The regression of character t on I is:

$$B_{G_t I} = \frac{Cov(G_t I)}{V(I)}$$

$$= \frac{\Sigma_i b_i G_{it}}{\Sigma_i \Sigma_j b_j a_i G_{ij}} ,$$

where t is the trait not included in the index, while i and j are traits which the index is based upon. Then, the indirect genetic response for the t^{th} trait (in the units of the trait) from the index selection based on other traits is:

$$\Delta G_t = k B_{G_t I} [V(I)]^{\frac{1}{2}}$$

$$= k \frac{Cov(G_t I)}{\sqrt{V(I)}}$$

$$= k \frac{\Sigma_i b_i G_{it}}{\sqrt{\Sigma_i \Sigma_j b_j a_i G_{ij}}} .$$

The assumptions involved in the construction of an index are:

1. The phenotypic value (X_i) of the i^{th} trait is the sum of the genotypic value (G_i) and the effects of environment (E_i) upon that trait, i.e., $X_i = G_i + E_i$.
2. There is no correlation (or covariance) between the genotypic values for any particular trait and the deviations due to environmental influences for that trait or for any other trait.
3. H and I are normally distributed with variances of σ^2_H and σ^2_I.
4. The quantitative variables G_i and X_i are linearly correlated.

Modified selection indices proposed by Pesek and Baker (1969) were considered as another procedure to improve several agronomic traits simultaneously. To use the proposed modification, two types of information are required: 1) the genetic variance-covariance matrix and 2) the vector of desired gains of the n traits. Their selection index is of the form

$$I = b_1{*}X_1 + b_2{*}X_2 + \cdots + b_n{*}X_n = \Sigma_i b_i{*}X_i$$

where the X_i's are the mean values of the traits for a particular individual and the $b_i{*}$'s are index coefficients. The values of $b_i{*}$'s, which will maximize the expected response to index selection in proportion to the desired response, can be computed from n simultaneous equations:

$$\begin{array}{llll} b_1{*}G_{11} & + b_2{*}G_{12} + \cdots & + b_n{*}G_{1n} & = h_1 \\ b_1{*}G_{21} & + b_2{*}G_{22} + \cdots & + b_n{*}G_{2n} & = h_2 \\ \vdots & \vdots & \vdots & \vdots \end{array}$$

$$b_1{*}G_{n1} + b_2{*}G_{n2} + \cdots b_n{*}G_{nn} = h_n$$

where b_j*'s are the index coefficients to be solved for, G_{ij} is the genotypic covariance between traits i and j, and h_i is the desired genetic gain for the i^{th} trait. The above equations can be reduced to a general form:

$$\Sigma_j b_j{*}G_{ij} = h_i,$$

where i is constant in each equation. The solution of these equations for b_j* is

$$b_j{*} = \Sigma_i D_{ij} h_i,$$

where the values of D_{ij} are given by the matrix

$$\begin{matrix} D_{11} & D_{12} & \cdots\cdots & D_{1n} \\ D_{21} & D_{22} & \cdots\cdots & D_{2n} \\ \vdots & \vdots & & \vdots \\ D_{n1} & D_{n2} & \cdots\cdots & D_{nn} \end{matrix},$$

which is the inverse of:

$$\begin{matrix} G_{11} & G_{12} & \cdots\cdots & G_{1n} \\ G_{21} & G_{22} & \cdots\cdots & G_{2n} \\ \vdots & \vdots & & \vdots \\ G_{n1} & G_{n2} & \cdots\cdots & G_{nn} \end{matrix}.$$

By using the relation $\Sigma_j b_j P_{ij} = \Sigma_j a_j G_{ij}$ of conventional theory and inserting the index coefficients (b_j*) and the phenotypic (P_{ij}) and genotypic (G_{ij}) variance-covariance matrices, it is possible to estimate the economic values (a_j^*) that would have resulted in identical expectations. The expected genetic responses from the use of modified index selection can be obtained by the same procedures as described before.

According to Pesek and Baker (1970), the application of the modified selection index does not result in total genetic improvement for all traits at once as specified by a breeder. In fact, it will result in smaller expected gains than desired. The expected gains per cycle of each trait will always be a constant multiple of the desired gains.

RESULTS AND DISCUSSION

Results reported herein were obtained from three years' experimentation. In 1974, I measured 288 S_1 lines in one-row plots. However, to facilitate more comprehensive characterization of the breeding population and to assure equal competition between plots, I measured more traits on fewer families (144 S_1 lines increased by sib-mating) in three-row plots in 1975 and 1976. Consequently, the three experiments were not identical and some traits were not measured every year (Table 2). Results from the 1974 experiment will be discussed separately, and because of the differences in experimental techniques, comparisons of the 1974 data with those from the 1975 and 1976 experiments should be interpreted with caution.

Since the major objectives of my study were to determine the relationships between several traits of BSUL1 and high-density yield performance, and to determine whether yield potential could be increased by improving traits related to yield and barrenness at high density, measurements at the high density are presented in the tables and discussed in the text before measurements at the low density.

Genotypic Variability in BSUL1

1974 experiment

Means and ranges for several traits of the 288 S_1 lines measured in 1974 suggested that at both plant densities large amounts of variability exist in BSUL1 (Table 7). Analyses of variance indicated

Table 7. Means and ranges for 18 traits of 288 random S_1 lines from BSUL1 grown at two plant densities in 1974

	101,600 pl/ha			40,640 pl/ha		
Traits	Mean	Range		Mean	Range	
YIELD (q/ha)	39.6	9.1 -	71.8	44.2	9.9 -	72.8
BARREN (%)	25.0	0.0 -	84.0	-[1]	-	-
PROLIF	-	-	-	97.1	40.0 -	162.0
GRNPLA (g/dm^2)	1.3	0.3 -	2.8	2.1	0.6 -	3.9
PTHT (cm)	-	-	-	152.7	122.0 -	199.4
ERHT (cm)	-	-	-	61.8	34.3 -	102.2
ERHT:PTHT	-	-	-	0.41	0.30 -	0.59
TBN	-	-	-	17.2	7.8 -	32.6
PLA (cm^2)	5063	3242	- 6637	5143	3799	- 6511
LOV_j	-	-	-	50.4	30.6 -	72.3
LOV_a	-	-	-	51.9	33.2 -	70.0
LOV_b	-	-	-	48.6	31.0 -	64.1
LOR_j	-	-	-	1.3	1.0 -	3.0
LOR_m	-	-	-	2.2	1.0 -	5.0
50%ANTH	24.0	17.3 -	31.9	-	-	-
50%SILK	28.6	21.3 -	37.0	-	-	-
PSS	4.6	0.4 -	11.1	-	-	-
SI	4.0	0.0 -	13.1	-	-	-

[1]Trait not measured.

highly significant differences among genotypes for all traits measured at both the high (Tables 8 and 9) and low plant densities (Tables 10, 11 and 12). Evidently, adequate variability exists within BSUL1 to permit successful selection for reduced barrenness and increased yield potential. Also, variability within the population should be sufficient to allow improvement of canopy orientation and reduced tassel size. The existence of these large amounts of variability may be explained by the fact that BSUL1 was derived from crosses between 16 parents of diverse origin (Table 1) and is an unimproved breeding population (i.e., has not been subjected to a recurrent population improvement program).

The lattice design used in the 1974 experiment was effective in removing within-replication variation; i.e., a significant block effect was obtained for 15 of the 21 traits I measured (Tables 8, 9, 10, 11 and 12). At the high plant density, highest lattice efficiencies (compared with a randomized block) were 159.1 and 122.5% for PLA and 50% ANTH, respectively. The highest efficiencies at the low density were 157.1, 156.1 and 129.6% for LOV_j, LOV_b and LOV_a, respectively.

Coefficients of variation (C.V.'s) larger than 20% were recorded for 5 of the 8 traits measured at the high density (Tables 8 and 9). High C.V.'s also were recorded for LOR, YIELD and GRNPLA at the low density (Tables 10 and 11). These high C.V.'s indicate that measurement techniques for these traits were not precise, and they may be attributed partly to use of one-row plots. If the stand in a high-density plot was poor, competition was reduced within that plot and within and between plots adjacent to the poor plot.

Table 8. Analyses of variance for barrenness and grain-yield traits of 288 S_1 lines from BSUL1 grown at 101,600 pl/ha in 1974

Source	df	Mean squares			
		YIELD	BARREN	GRNPLA	PLA
Sets (s)	1	26.2	3.2	2.450**	8005363**
Replicates/s	2	1332.1	145.7	0.904	6629008
Genotypes/s	286	294.7**	451.8**	0.291**	537978**
Blocks/s	44	174.4**	308.1**	0.146*	1000011**
Pooled effective error	242	77.3	151.4	0.095	179685
Lattice efficiency (%)		108.5	108.4	101.6	159.1
C.V. (%)		22.2	48.9	27.0	8.4

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 9. Analyses of variance for flowering traits of 288 S_1 lines from BSUL1 grown at 101,600 pl/ha in 1974

Source	df	Mean squares			
		50%ANTH	50%SILK	PSS	SI
Sets (s)	1	0.64	19.16*	11.40*	0.01
Replicates/s	2	5.72	37.61	67.08	24.13
Genotypes/s	286	8.94**	20.22**	8.83**	9.11**
Blocks/s	44	4.25**	6.50**	3.79*	4.87
Pooled effective error	242	1.41	4.05	2.70	4.99
Lattice efficiency (%)		122.5	104.3	102.2	100.1
C.V. (%)		5.0	7.0	36.1	56.7

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 10. Analyses of variance for prolificacy and grain-yield traits of 288 S_1 lines from BSUL1 grown at 40,640 pl/ha in 1974

Source	df	Mean squares YIELD	PROLIF	GRNPLA
Sets (s)	1	705.8*	2871.1**	1.57*
Replicates/s	2	3529.5	1332.1	0.77
Genotypes/s	286	230.2**	608.3**	0.52**
Blocks/s	44	210.7**	277.5	0.24
Pooled effective error	242	109.2	319.1	0.24
Lattice efficiency (%)		108.3	100.0	100.0
C.V. (%)		23.6	18.4	24.1

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 11. Analyses of variance for canopy-orientation traits of 288 S_1 lines from BSUL1 grown at 40,640 pl/ha in 1974

Source	df	Mean squares				
		LOV_j	LOV_a	LOV_b	LOR_j	LOR_m
Sets (s)	1	5623.8**	1381.4**	1537.3**	0.32	4.88**
Replicates/s	2	11083.8	4911.3	6348.1	0.12	1.80
Genotypes/s	286	111.6**	74.7**	71.3**	0.29**	1.12**
Blocks/s	44	308.8**	105.5**	154.2**	0.10	0.47
Pooled effective error	242	57.7	31.2	29.7	0.09	0.40
Lattice efficiency (%)		157.1	129.6	156.1	100.6	101.3
C.V. (%)		15.2	10.8	11.2	22.6	27.8

**Significant at the 1% level of probability.

Table 12. Analyses of variance for plant traits of 288 S_1 lines from BSUL1 grown at 40,640 pl/ha in 1974

		Mean squares				
Source	df	PTHT	ERHT	ERHT:PTHT	TBN	PLA
Sets (s)	1	2316.0**	511.9**	0.0010	127.01	212636
Replicates/s	2	3897.6	630.1	0.0051	13.47	2279979
Genotypes/s	286	429.7**	241.6**	0.0049**	46.60**	522469**
Blocks/s	44	166.7**	85.1**	0.0028**	7.21	527033**
Pooled effective error	242	63.8	42.7	0.0014	6.66	260167
Lattice efficiency (%)		117.9	109.8	108.6	100.4	111.0
C.V. (%)		5.2	10.5	9.2	15.0	10.0

**Significant at the 1% level of probability.

Because of the problems encountered in 1974 and in an attempt to increase the precision of the experiment, I decided to grow the 1975 and 1976 experiments in three-row plots and to reduce the number of lines to one set of 144.

Excluding random chance, theoretically, the difference between sets should be due only to the environment because each set was composed of random lines. I found significant differences between sets, however, for GRNPLA, PLA, 50%SILK and PSS at the high density and for YIELD, PROLIF, GRNPLA, LOR_m, all LOV measurements, PTHT and ERHT at the low density (Tables 8, 9, 10, 11 and 12). Means for each trait in each set are shown in Table 13. Set 2 had more upright canopy orientations during grain filling (LOV_a, LOV_b and LOR_m), displayed more prolificacy, had smaller tassels and possessed shorter pollen-shed-to-silking intervals than Set 1. Since these traits have been associated with tolerance to high plant densities (Buren, 1970), I decided to study Set 2 exclusively in 1975 and 1976.

<u>1975-1976 experiments</u>

Similar to the results obtained in 1974, means and ranges for several traits of the 144 S_1 families grown in 1975 and 1976 suggested that large amounts of variability exist in BSUL1 (Table 14). Although the mean yield at the low plant density was only 5.2 q/ha higher than the yield at the high plant density, yield per plant (YIELDP) was 2.2 times greater at the low density indicating that 96,875 pl/ha provided a stress environment for BSUL1. Plants grown at 96,875 pl/ha flowered later, exhibited a longer flowering duration, were slightly taller with

Table 13. Means for 18 traits of two sets of 144 random S_1 lines from BSUL1 grown at two plant densities in 1974

Traits	101,600 pl/ha		40,640 pl/ha	
	Set 1	Set 2	Set 1	Set 2
YIELD (q/ha)	39.8	39.4	45.3	43.1
BARREN (%)	25.0	24.9	-[1]	-
PROLIF	-	-	94.8	99.3
GRNPLA (g/dm^2)	1.3	1.2	2.1	2.0
PTHT (cm)	-	-	154.7	150.7
ERHT (cm)	-	-	62.7	60.8
ERHT:PTHT	-	-	0.4	0.4
TBN	-	-	17.6	16.7
PLA (cm^2)	4946	5181	5105	5143
LOV_j	-	-	53.5	47.2
LOV_a	-	-	50.3	53.4
LOV_b	-	-	46.9	50.2
LOR_j	-	-	1.3	1.3
LOR_m	-	-	2.1	2.3
50%ANTH	24.0	24.0	-	-
50%SILK	28.8	28.4	-	-
PSS	4.7	4.4	-	-
SI	3.9	4.0	-	-

[1]Trait not measured.

Table 14. Means and ranges for 27 traits of 144 S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

	96,875 pl/ha		42,383 pl/ha	
Traits	Mean	Range	Mean	Range
YIELD (q/ha)	38.3	11.8 - 67.7	43.5	21.0 - 65.2
YIELDP (g)	42.7	16.2 - 74.3	93.0	93.0 - 138.2
BARREN (%)	35.5	6.8 - 76.2	13.2	0.0 - 42.9
PROLIF	64.8	23.9 - 96.7	91.2	57.1 - 125.6
SECOND (%)	-[2]	- -	1.9	0.0 - 12.9
GRNPLA[1] (g/dm^2)	0.9	0.2 - 1.8	1.8	1.0 - 2.9
LODG (%)	20.8	0.0 - 72.7	14.6	0.0 - 63.9
STAND	26.0	19.8 - 28.7	9.6	8.2 - 10.0
PTHT (cm)	162.9	132.8 - 201.8	161.1	129.3 - 197.4
ERHT (cm)	76.8	58.8 - 101.9	72.7	54.4 - 107.9
ERHT:PTHT	0.46	0.37 - 0.55	0.45	0.37 - 0.55
TBN	16.2	4.8 - 31.7	16.5	6.9 - 29.8
LOV_j[1]	56.7	44.5 - 70.1	56.0	42.4 - 68.1
LOV_a	50.6	29.6 - 64.3	50.9	28.5 - 62.5
LOV_b[1]	48.1	31.5 - 63.2	46.5	29.0 - 62.4
LOR_j[1]	-	- -	1.6	0.9 - 3.1
LOR_m	-	- -	2.0	0.9 - 4.0
PLA[1] (cm^2)	5328	4169 - 6697	6029	4593 - 8009
25%ANTH (days)	22.7	15.5 - 28.7	21.9	15.9 - 28.3
50%ANTH (days)	24.7	17.3 - 30.0	23.7	17.0 - 28.8
75%ANTH (days)	26.4	18.9 - 32.1	25.3	18.2 - 30.8
25%SILK (days)	26.8	19.2 - 35.2	24.5	17.2 - 30.1
50%SILK (days)	30.3	21.3 - 42.0	26.9	19.3 - 36.6
75%SILK (days)	34.3	23.8 - 45.4	29.9	20.7 - 41.6
PSS (days)	5.5	0.6 - 12.6	3.2	-0.5 - 9.1
SI (days)	7.5	3.1 - 16.5	5.5	2.5 - 14.8
SD (days)	6.4	1.1 - 12.6	3.9	0.1 - 9.3

[1]Measured in 1975 only.

[2]Trait not measured.

higher ear placement and displayed smaller leaf area than plants grown at 42,383 pl/ha. Seventeen of the 24 traits common to both densities exhibited a greater range at the high density; therefore, 96,875 pl/ha provided a better environment for determining differences among families for traits I measured.

Estimates of variance components and heritabilities (Tables 15, 16, 17 and 18) indicated the majority of the variability in BSUL1 was genotypic. Heritability estimates ranged from 0.14 for GRNPLA (low density) to 0.91 for both TBN (low density) and 25%ANTH (high density). All heritabilities for barrenness and grain-yield traits (Table 15) were larger at the high than at the low plant density. Furthermore, the heritability estimate for GRNPLA at 42,383 pl/ha (0.14±0.14) was not significantly different from zero. The heritability estimate for LODG was also greater at the high than the low density but heritability for TBN was greater at the low density (Table 18). Differences in heritability estimates between densities were small for all other traits. Generally, heritability estimates for physiological traits influencing maturity (i.e., ANTH and SILK) and for morphological traits (i.e., PTHT, ERHT, TBN and LOV_a) were greater than those for barrenness and grain-yield traits.

Analyses of variance showed highly significant genotypic differences for all traits at both densities (Tables 19 through 27). Additionally, many traits exhibited a significant genotype x environment interaction (G x E), indicating they should be evaluated in more than one environment. Some plant traits (PTHT, ERHT, ERHT:PTHT, TBN and LOV_a at high density;

Table 15. Genotypic variances (V_g), genotype x environment interaction variances (V_{ge}), heritability estimates (h^2) and standard errors for barrenness and grain-yield traits of 144 S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

Traits	96,875 pl/ha			42,383 pl/ha		
	V_g	V_{ge}	h^2	V_g	V_{ge}	h^2
YIELD	88.4 ±15.3	35.3 ± 9.2	0.71±0.05	33.9 ± 8.5	26.6 ± 8.0	0.52±0.08
YIELDP	104.9 ±17.7	41.7 ±11.6	0.70±0.05	139.6 ±38.4	141.5 ±38.3	0.48±0.09
BARREN	183.7 ±29.2	46.5 ± 7.5	0.76±0.04	35.1 ±11.1	23.6 ±12.7	0.43±0.09
PROLIF	186.3 ±29.6	47.2 ±15.4	0.76±0.04	72.5 ±18.0	39.8 ±17.5	0.52±0.08
SECOND	-[b]	-	-	3.65± 1.02	1.34± 1.12	0.48±0.09
GRNPLA[a]	0.02± 0.01	0.06± 0.01	0.31±0.11	0.02± 0.02	0.11± 0.03	0.14±0.14

[a]Measured in 1974 and 1975.

[b]Trait not measured.

Table 16. Genotypic variances (V_g), genotype x environment interaction variances (V_{ge}), heritability estimates (h^2) and standard errors for traits measuring flowering date and duration of 144 S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

Traits	96,875 pl/ha			42,383 pl/ha		
	V_g	V_{ge}	h^2	V_g	V_{ge}	h^2
25%ANTH	4.12±0.54	0.05±0.12	0.91±0.02	3.69±0.49	0.11±0.12	0.89±0.02
50%ANTH	4.14±0.55	0.29±0.14	0.90±0.02	3.85±0.50	0.02±0.12	0.90±0.02
75%ANTH	4.43±0.60	0.23±0.18	0.87±0.02	4.05±0.54	0.08±0.16	0.88±0.02
25%SILK	7.74±1.03	0.31±0.28	0.89±0.02	6.17±0.82	0.32±0.21	0.89±0.02
50%SILK	14.01±1.97	2.41±0.65	0.85±0.03	7.56±1.04	0.93±0.32	0.86±0.02
75%SILK	20.61±3.05	2.99±1.31	0.81±0.02	11.20±1.70	0.64±0.84	0.79±0.04
PSS	5.46±0.93	2.08±0.55	0.71±0.05	1.71±0.33	0.90±0.24	0.64±0.06
SI	5.20±1.12	1.30±1.00	0.59±0.07	2.23±0.53	0.00±0.58	0.54±0.04
SD	4.70±0.78	1.30±0.45	0.73±0.04	2.68±0.42	0.66±0.21	0.77±0.04

Table 17. Genotypic variances (V_g), genotype x environment interaction variances (V_{ge}), heritability estimates (h^2) and standard errors for canopy-orientation traits of 144 S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

Traits	96,875 pl/ha			42,383 pl/ha		
	V_g	V_{ge}	h^2	V_g	V_{ge}	h^2
LOV_j[1]	11.68±3.56	-[2]	0.55±0.04	7.76 ±3.40	13.08 ±4.20	0.32±0.11
LOV_a	39.49±6.21	1.35±3.49	0.77±0.04	38.38 ±5.99	7.11 ±2.84	0.77±0.04
LOV_b[1]	31.03±7.90	-	0.65±0.03	22.56 ±3.94	5.07 ±2.58	0.70±0.05
LOR_j	-	-	-	0.096±0.02	0.023±0.01	0.72±0.05
LOR_m	-	-	-	0.189±0.04	0.068±0.037	0.58±0.07

[1] Measured at low density in 1974 and 1975 and at high density in 1975 only.

[2] Trait not measured.

Table 18. Genotypic variances (V_g), genotype x environment interaction variances (V_{ge}), heritability estimates (h^2) and standard errors for plant traits of 144 S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

Traits	96,875 pl/ha			42,383 pl/ha		
	V_g	V_{ge}	h^2	V_g	V_{ge}	h^2
ERHT	54.86± 8.21	0.15± 4.05	0.80±0.03	65.26± 9.58	7.89± 4.03	0.81±0.01
PTHT	128.22±19.01	4.35± 8.86	0.81±0.03	148.8 ±21.0	10.5 ± 6.6	0.84±0.03
ERHT:PTHT	0.76± 0.14[a]	0.08± 0.10[a]	0.68±0.05	0.94± 0.17[a]	0.25± 0.12[a]	0.69±0.05
PLA[b]	70465 ±19784	37543±21393	0.47±0.09	62649 ±20915	13009±26144	0.41±0.10
TBN	17.45± 2.70	1.16± 1.43	0.78±0.04	19.96± 2.59	0.35± 0.58	0.91±0.02
LODG	167.35±27.68	60.66±15.20	0.73±0.04	80.70±20.41	81.60±18.87	0.52±0.08

[a]To obtain actual value multiply by 10^{-3}.

[b]Measured in 1974 and 1975.

Table 19. Analyses of variance for barrenness and grain-yield traits of 144 S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Source	df	Mean squares				
		YIELD	YIELDP	BARREN	PROLIF	GRNPLA[a]
Environments (E)	1	12004.2**	5712.5**	872.5	1163.0*	13.66**
Replicates/E	2	886.1	1495.4	1381.7	1417.1	0.07
Genotypes (G)	143	499.2**	601.2**	966.2**	980.3**	0.26**
G x E	143	145.6**	181.6**	231.6**	235.0**	0.18**
Pooled error						
Randomized block	286	84.8	111.1	143.6	145.1	0.07
Effective	242	75.0	98.2	138.5	140.6	0.07

[a]Measured in 1974 and 1975.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 20. Analyses of variance for plant traits of 144 S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Source	df	Mean squares					
		PTHT	ERHT	ERHT:PTHT	TBN	PLA[a]	LODG
Environments (E)	1	223568.9**	179633.6**	1.7052**	153.02**	12371191**	7920.9**
Replicates/E	2	13355.7	3583.5	0.0098	24.30	7695023	1372.9
Genotypes (G)	143	635.6**	274.2**	0.0045**	89.89**	596084**	911.2**
G x E	143	122.7	54.8	0.0014	20.06	314223*	241.8**
Pooled error							
Randomized block	286	145.7	57.9	0.0013	17.92	271482	120.4
Effective	242	114.0	54.5	0.0013	17.75	239136	120.5

[a]Measured in 1974 and 1975.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 21. Analyses of variance for days to anthesis and silk-emergence of 144 S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Source	df	Mean squares					
		25%ANTH	50%ANTH	75%ANTH	25%SILK	50%SILK	75%SILK
Environments (E)	1	400.67**	498.62**	154.44**	259.22**	390.60**	25.59
Replicates/E	2	5.35	9.84	6.92	5.09	2.19	0.56
Genotypes (G)	143	18.17**	18.62**	20.30**	34.92**	66.28**	102.05**
G x E	143	1.68	2.07**	2.57*	3.95	10.24**	19.60**
Pooled error							
Randomized block	286	1.75	1.79	2.57	3.63	5.82	13.53
Effective	242	1.59	1.48	2.11	3.38	5.42	13.63

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 22. Analyses of variance for flowering-duration and canopy-orientation traits of 144 S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Source	df	Mean squares PSS	SI	SD	LOV_a
Environments (E)	1	3.13	128.91**	6.71	674.7**
Replicates/E	2	4.45	13.14	8.73	492.1
Genotypes (G)	143	30.57**	35.20**	25.72**	206.1**
G x E	143	8.73**	14.41*	6.92**	48.1
Pooled error					
Randomized block	286	4.58	11.81	4.20	45.9
Effective	242	4.56	11.81	4.31	45.4

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 23. Analyses of variance for barrenness and grain-yield traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Source	df	Mean squares					
		YIELD	YIELDP	PROLIF	SECOND	GRNPLA[a]	BARREN
Environments (E)	1	45966.7**	164631.6**	5010.1**	9.51	2.10*	3869.8**
Replicates/E	2	187.1	1007.4	287.9	0.97	0.99	79.4
Genotypes (G)	143	259.9**	1162.1**	552.6**	30.65**	0.47**	327.8**
G x E	143	124.3**	603.6**	262.5**	16.07	0.40**	187.2**
Pooled error							
Randomized block	286	73.9	336.9	183.3	13.62	0.18	140.1
Effective	242	71.1	320.5	183.0	13.40	0.18	139.9

[a]Measured in 1974 and 1975.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 24. Analyses of variance for plant traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

		Mean squares					
Source	df	PTHT	ERHT	ERHT:PTHT	TBN	PLA[a]	LODG
Environments (E)	1	191842.0**	185113.9**	2.2713**	21.30	112925648**	11908.2**
Replicates/E	2	7324.6	4429.2	0.8310	2.97	109526	6.9
Genotypes	143	705.2**	320.9**	0.0055**	87.97**	613170**	625.6**
G x E	143	109.9*	59.8**	0.0017**	8.11	362570	302.8**
Pooled error							
Randomized block	286	94.8	49.4	0.0014	7.73	351104	141.1
Effective	242	88.9	44.0	0.0012	7.41	336552	139.6

[a]Measured in 1974 and 1975.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 25. Analyses of variance for days to anthesis and silk-emergence of 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Source	df	Mean squares					
		25%ANTH	50%ANTH	75%ANTH	25%SILK	50%SILK	75%SILK
Environments (E)	1	550.06**	687.80**	409.15**	303.27**	237.47**	43.37
Replicates/E	2	20.86	17.71	24.33	25.43	30.78	15.74
Genotypes (G)	143	16.51**	17.07**	18.37**	27.71**	35.13**	56.57**
G x E	143	1.75	1.67	2.18	3.03*	4.90**	11.76
Pooled error							
Randomized block	286	1.74	1.82	2.16	2.70	3.49	10.49
Effective	242	1.53	1.64	2.02	2.39	3.05	10.49

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 26. Analyses of variance for flowering-duration traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Source	df	Mean squares PSS	SI	SD
Environments (E)	1	118.53**	624.99**	179.56**
Replicates/E	2	3.04	2.02	0.30
Genotypes (G)	143	10.63**	16.55**	3.99**
G x E	143	3.79**	7.62	3.26**
Pooled error				
Randomized block	286	1.08	8.05	1.92
Effective	242	2.00	8.07	1.93

**Significant at the 1% level of probability.

Table 27. Analyses of variance for canopy-orientation traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

		Mean squares				
Source	df	LOV_j[1]	LOV_a	LOV_b[1]	LOR_j[1]	LOR_m
Environments (E)	1	10981.2**	840.7**	1946.4**	15.67**	0.50
Replicates/E	2	8018.4	469.2	962.0	0.51	0.74
Genotypes (G)	143	96.0**	198.8**	128.6**	0.53**	1.30**
G x E	143	64.9**	45.3**	38.3**	0.15**	0.54**
Pooled error						
Randomized block	286	60.4	31.3	38.5	0.11	0.41
Effective	242	38.8	31.1	28.2	0.11	0.41

[1]Measured in 1974 and 1975.

**Significant at the 1% level of probability.

TBN and PLA at low density), flowering traits (25%ANTH and 25%SILK at high density; 25%, 50% and 75%ANTH, 75%SILK and SI at low density) and SECOND, however, did not display significant G x E interactions. Standard errors indicated that G x E variance components for these traits were not significantly greater than zero (Tables 16, 17 and 18).

Genotypic variances were larger than G x E variances for 42 of the 47 traits I measured (Tables 15, 16, 17 and 18). The only traits that did not display this phenomenon were YIELDP, GRNPLA, LODG and LOV_j at the low density and GRNPLA at high density. In general, the G x E variances, when expressed as percentages of the genotypic variances, were greatest for barrenness and grain-yield traits. The G x E variances for YIELD were 39.9 and 78.5% as large as the genotypic variances at high and low densities, respectively. The G x E variances for TBN, however, were only 6.6 and 1.8% as large as the genotypic variances at the respective densities. The magnitudes of the G x E variances relative to those of the genotypic variances were relatively small for plant and flowering traits; therefore, it may be possible to select for these traits in one environment. Selection for reduced barrenness, improved yield traits, lodging resistance and leaf area per plant, however, may need to be conducted in more than one environment to minimize bias from G x E.

Analyses of traits across plant densities in 1975 and 1976, supported conclusions drawn from the preliminary experiment conducted in 1974; i.e., adequate genotypic variability existed in BSUL1 to permit successful selection for reduced barrenness and increased yield potential. Furthermore, variability within the population was sufficient to permit successful improvement of canopy orientation and reduction of tassel size.

Correlations

To provide indications of the relative importance of various traits in the determination of barrenness and/or grain yield and to determine the relationships among the traits, I computed adjusted phenotypic correlations between all traits at both plant densities. Three general conclusions were drawn from these data: 1) YIELDP, BARREN, PROLIF, GRNPLA, SECOND and all flowering traits were highly correlated with YIELD (especially at the high density) and thus were important in determining grain yield (Tables 28 and 29). Significant but smaller correlations between YIELD and TBN, PLA, LODG, ERHT, PTHT and ERHT:PTHT ratio indicated that these plant traits may be of secondary importance in determining grain yield, 2) with the exception of PTHT, ERHT and PLA, traits significantly correlated with YIELD at the high plant density invariably were significantly correlated at the low density. The magnitudes of the correlation coefficients at the low, however, were not as large as they were at the high density; e.g., the r-value between YIELD and SI at the high density was -0.69 (Table 28) and at the low density it was -0.51 (Table 29), 3) several traits measured at low density were significantly correlated with YIELD and BARREN at high density, but these r-values generally were smaller than those for the same correlations at the high density (Tables 28 and 29). For example, the correlation between YIELD and SD at the high density was -0.71 (Table 28) and the correlation between YIELD (high density) and SD (low density) was -0.58 (Table 29). Perhaps performance at a low density can be used as an indicator of performance at a high density. The r-values between

Table 28. Adjusted phenotypic correlations for grain yield and barrenness with all traits measured at 96,875 pl/ha

	96,875 pl/ha		42,383 pl/ha	
Traits	YIELD	BARREN	YIELD	BARREN
YIELD	1.00**	-0.88**	0.75**	-0.59**
YIELDP	0.98**	-0.89**	0.74**	-0.59**
BARREN	-0.88**	1.00**	-0.62**	0.66**
PROLIF	0.88**	-0.99**	0.62**	-0.66**
GRNPLA	0.70**	-0.66**	0.46**	-0.39**
PTHT	0.01	0.12	0.14	0.02
ERHT	0.10	-0.04	0.22**	-0.07
ERHT:PTHT	0.15	-0.20*	0.21**	-0.15
TBN	-0.23**	0.22**	-0.09	0.11
PLA	-0.18*	0.22**	-0.10	0.16
LODG	0.26**	-0.29**	0.29**	-0.27**
LOV_j	0.15	-0.11	0.14	-0.11
LOV_a	-0.05	0.10	-0.04	0.15
LOV_b	-0.01	0.10	0.08	0.01
25%ANTH	-0.34**	0.41**	-0.18*	0.20*
50%ANTH	-0.34**	0.43**	-0.18*	0.21**
75%ANTH	-0.33**	0.42**	-0.18*	0.22**
25%SILK	-0.58**	0.61**	-0.38**	0.40**
50%SILK	-0.66**	0.73**	-0.47**	0.51**
75%SILK	-0.73**	0.80**	-0.53**	0.58**
PSS	-0.70**	0.74**	-0.55**	0.60**
SI	-0.69**	0.79**	-0.53**	0.60**
SD	-0.71**	0.73**	-0.57**	0.61**

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 29. Adjusted phenotypic correlations for grain yield and barrenness with all traits measured at 42,383 pl/ha

	96,875 pl/ha		42,383 pl/ha	
Traits	YIELD	BARREN	YIELD	BARREN
YIELD	0.75**	-0.62**	1.00**	-0.71**
YIELDP	0.74**	-0.63**	0.97**	-0.73**
BARREN	-0.59**	0.66**	-0.71**	1.00**
PROLIF	0.63**	-0.68**	0.73**	-0.87**
SECOND	0.40**	-0.31**	0.38**	-0.24**
GRNPLA	0.53**	-0.44**	0.68**	-0.50**
PTHT	-0.01	0.10	0.19*	-0.04
ERHT	0.10	-0.04	0.24**	-0.13
ERHT:PTHT	0.14	-0.16	0.18	-0.18*
TBN	-0.26**	0.22**	-0.16*	0.11
PLA	-0.11	0.14	0.02	0.10
LODG	0.15	-0.19*	0.16*	-0.15
LOV_j	0.02	-0.03	0.03	0.00
LOV_a	-0.05	0.08	-0.04	0.10
LOV_b	-0.01	0.08	0.01	0.10
LOR_j	0.09	-0.11	0.06	-0.07
LOR_m	0.15	-0.08	0.19*	-0.07
25%ANTH	-0.31**	0.39**	-0.19*	0.18*
50%ANTH	-0.34**	0.41**	-0.20*	0.20*
75%ANTH	-0.35**	0.42**	-0.24**	0.22**
25%SILK	-0.48**	0.53**	-0.34**	0.35**
50%SILK	-0.51**	0.56**	-0.39**	0.41**
75%SILK	-0.59**	0.66**	-0.49**	0.55**
PSS	-0.48**	0.49**	-0.44**	0.48**
SI	-0.49**	0.55**	-0.51**	0.62**
SD	-0.58**	0.60**	-0.55**	0.61**

*,**Significant at the 5% and 1% levels of probability, respectively.

densities were similar whether the traits were significantly correlated (i.e., YIELD and BARREN) or not (i.e., YIELD and LOV_a). My results are consistent with those obtained for several single-cross hybrids by Buren (1970) and Buren et al. (1974).

With the exception of LOR_m, canopy-orientation traits were not correlated with YIELD or BARREN at either density (Tables 28 and 29). Crosbie (1976) observed similar results, but Pepper (1974) and Mulamba (1977) reported significant relationships between canopy orientation and grain yield of maize at high plant densities. Perhaps my non-significant correlations were a consequence of testing in wide-row spacings (102 cm), because canopy orientation should be more important in narrow-row conditions (Mock and Pearce, 1975). My analysis suggested that canopy-orientation traits would be of minor importance in improving grain-yield potential of BSUL1.

Correlations between BARREN and ERHT:PTHT and BARREN and LODG were -0.20* and -0.29**, respectively, suggesting a reduction in barrenness (and subsequent increase in yield) may be accompanied by an agronomically unacceptable higher ear placement and increased lodging. Selection for reduced barrenness, therefore, should also be accompanied by selection for improved plant traits.

Grain-yield traits, barrenness and flowering traits were all highly correlated suggesting that improvement of one trait should result in improvement of the other. However, some traits require tedious measurements (e.g., GRNPLA, SI and SD). Conversely, measurement of prolificacy (PROLIF) is relatively simple. Adjusted phenotypic correlations between

PROLIF and GRNPLA, 75%SILK, PSS, SI and SD at 96,875 pl/ha were 0.66, -0.80, -0.74, -0.79 and -0.73, respectively (Appendix Table 9). Additionally, r-values between PROLIF (low density) and the same traits at the high density were 0.44, -0.55, -0.59, -0.59 and -0.62, respectively (Appendix Table 11). Therefore, improvement of grain-yield potential and reduced barrenness resulting from favorable changes in flowering traits, may be achieved most simply by selection for increased prolificacy at a low density.

Genotypic correlations should verify genetic associations of various traits with grain yield and barrenness and ultimately should provide information useful in developing a selection index for improved yield potential. Strong genotypic associations of both BARREN and YIELD with YIELDP, PROLIF, SECOND, GRNPLA and all flowering traits at both plant densities were observed (Tables 30 and 31), suggesting that selection for these traits should ultimately improve the performance of BSUL1. Plant traits (TBN, PLA, LODG and ERHT:PTHT) and canopy-orientation traits (LOV_a and LOR_m) were of minor importance; whereas, PTHT, ERHT, LOV_j, LOV_b and LOR_j displayed the weakest associations with YIELD and BARREN.

Genotypic correlations at both densities were greater for flowering traits vs. BARREN than for the same traits vs. YIELD (Tables 30 and 31). At the low density, however, genotypic correlations for all plant traits with YIELD were larger than they were with BARREN (Table 31). Selection for improved flowering traits, therefore, should be more effective in reducing barrenness than in improving grain yield *per se*; but, selection for improved plant traits at a low plant density should be more effective

Table 30. Genotypic correlations for grain yield and barrenness with all traits measured at 96,875 pl/ha

	96,875		42,383 pl/ha	
Traits	YIELD	BARREN	YIELD	BARREN
YIELD	1.00	-0.90	0.97	-0.93
YIELDP	0.96	-0.90	0.98	-0.96
BARREN	-0.90	1.00	-0.80	0.98
PROLIF	0.69	-0.82	0.80	-0.97
GRNPLA	0.98	-0.90	0.49	-0.91[1]
PTHT	-0.10	0.23	0.04	0.14
ERHT	0.13	0.02	0.27	0.03
ERHT:PTHT	0.30	-0.29	0.41	-0.16
TBN	-0.28	0.28	-0.21	0.21
PLA	-0.32	0.37	-0.02	0.64[1]
LODG	0.43	-0.35	0.52	-0.49
LOV_j[1]	0.11	-0.03	0.05	-0.08
LOV_a	-0.08	0.14	-0.08	0.26
LOV_b[1]	0.03	0.08	0.04	-0.09
25%ANTH	-0.39	0.47	-0.21	0.29
50%ANTH	-0.36	0.46	-0.26	0.31
75%ANTH	-0.42	0.51	-0.26	0.34
25%SILK	-0.63	0.65	-0.50	0.59
50%SILK	-0.73	0.80	-0.62	0.75
75%SILK	-0.71	0.77	-0.60	0.76
PSS	-0.85	0.87	-0.65	0.95
SI	-0.85	0.96	-0.77	1.02
SD	-0.81	0.81	-0.84	1.02

[1]Measured in one year only.

Table 31. Genotypic correlations for grain yield and barrenness with all traits measured at 42,383 pl/ha

Traits	96,875 pl/ha		42,383 pl/ha	
	YIELD	BARREN	YIELD	BARREN
YIELD	0.97	-0.80	1.00	-0.87
YIELDP	0.94	-0.79	1.00	-0.88
BARREN	-0.93	0.98	-0.87	1.00
PROLIF	0.88	-0.82	0.87	0.95
SECOND	0.51	-0.42	0.62	-0.48
GRNPLA	0.96	-0.56	1.09	-0.88[1]
PTHT	-0.10	0.17	0.14	-0.02
ERHT	0.11	-0.04	0.27	-0.18
ERHT:PTHT	0.21	-0.20	0.27	-0.26
TBN	-0.30	0.24	-0.18	0.14
PLA	-0.10	0.25	-0.36	0.36[1]
LODG	0.35	-0.31	0.50	-0.32
LOV_j	0.01	0.01	-0.24	-0.19[1]
LOV_a	-0.14	0.13	-0.17	0.29
LOV_b	0.01	0.06	-0.01	-0.10[1]
LOR_j	0.03	-0.03	-0.08	-0.16[1]
LOR_m	0.23	-0.19	0.30	-0.24
25%ANTH	-0.40	0.47	-0.17	0.24
50%ANTH	-0.44	0.49	-0.20	0.26
75%ANTH	-0.43	0.52	-0.28	0.32
25%SILK	-0.62	0.63	-0.42	0.51
50%SILK	-0.80	0.67	-0.50	0.55
75%SILK	-0.78	0.80	-0.65	0.75
PSS	-0.72	0.67	-0.72	0.71
SI	-0.91	0.78	-0.80	0.87
SD	-0.74	0.70	-0.76	0.85

[1]Measured in one year only.

in improving grain yield per se than in reducing barrenness. Differences between plant densities for correlations of YIELD and BARREN with barrenness, grain-yield and canopy-orientation traits were small (Tables 30 and 31). Selection for improvement of these traits at either density, therefore, should result in similar improvement of grain yield per se and reduction of barrenness.

Genotypic correlations between all traits measured at the low density with YIELD and BARREN measured at the high density were slightly smaller than the correlations among these traits when all were measured at the high density (Tables 30 and 31). These data indicated that even though most improvement for high-density tolerance would be obtained with selection at high plant densities, selection could be conducted at lower densities with only a small sacrifice in rate of improvement.

Error correlations for several traits with YIELD and BARREN at both densities are presented in Tables 32 and 33. These correlations provide indications of the relative degree of common error between traits. The correlations of YIELD and BARREN with YIELD, YIELDP, BARREN, PROLIF, SECOND and GRNPLA were relatively high when measured at the same density, suggesting common errors were associated with their measurements. Since these measurements were all taken at harvest and since they are closely related to grain yield, high error correlations among these traits should be expected.

Error correlations of flowering, plant and canopy-orientation traits with YIELD and BARREN were relatively small (absolute values ranged from 0.00 to 0.42). Additionally, error correlations for traits measured at one density with YIELD and BARREN measured at the other density usually

Table 32. Error correlations for grain yield and barrenness with all traits measured at 96,875 pl/ha

Traits	96,875 pl/ha		42,383 pl/ha	
	YIELD	BARREN	YIELD	BARREN
YIELD	1.00	-0.69	0.29	-0.08
YIELDP	0.94	-0.74	0.25	-0.08
BARREN	-0.69	1.00	-0.15	0.04
PROLIF	0.37	-0.43	0.16	-0.05
GRNPLA	0.66	-0.60	0.15	-0.11[1]
PTHT	0.31	-0.13	0.13	0.03
ERHT	0.24	-0.17	0.09	0.02
ERHT:PTHT	0.05	-0.12	0.02	-0.05
TBN	0.04	0.00	0.01	0.04
PLA	-0.04	0.01	-0.05	-0.06[1]
LODG	0.05	-0.10	-0.07	0.06
LOV_j[1]	0.07	-0.09	0.22	-0.16
LOV_a	-0.08	0.10	-0.05	-0.03
LOV_b[1]	-0.10	0.05	-0.04	0.02
25%ANTH	0.02	-0.01	0.03	-0.04
50%ANTH	-0.07	0.08	-0.01	0.05
75%ANTH	-0.13	0.11	0.00	0.02
25%SILK	-0.22	0.08	-0.08	0.00
50%SILK	-0.32	0.26	-0.09	0.04
75%SILK	-0.30	0.25	-0.05	-0.02
PSS	-0.31	0.25	-0.09	0.03
SI	-0.20	0.21	-0.01	-0.03
SD	-0.37	0.33	0.00	-0.09

[1]Measured in one year only.

Table 33. Error correlations for grain yield and barrenness with all traits measured at 42,383 pl/ha

	96,875 pl/ha		42,383 pl/ha	
Traits	YIELD	BARREN	YIELD	BARREN
YIELD	0.29	-0.15	1.00	-0.52
YIELDP	0.29	-0.18	0.91	-0.57
BARREN	-0.08	0.04	-0.52	1.00
PROLIF	0.19	-0.15	0.54	-0.81
SECOND	0.15	-0.13	0.75	0.07[1]
GRNPLA	0.26	-0.12	0.82	-0.54
PTHT	0.24	-0.07	0.19	0.00
ERHT	0.09	0.01	0.10	-0.01
ERHT:PTHT	-0.06	0.01	-0.01	-0.02
TBN	0.10	-0.09	-0.05	0.08
PLA	-0.01	-0.05	-0.05	0.03[1]
LODG	-0.08	0.11	-0.04	-0.05
LOV_j	0.04	0.08	-0.10	-0.01[1]
LOV_a	0.07	-0.08	-0.08	-0.03
LOV_b	0.10	-0.03	-0.01	0.06[1]
LOR_j	-0.02	0.00	0.11	-0.11[1]
LOR_m	0.05	0.00	-0.02	0.02
25%ANTH	0.03	0.09	-0.03	0.03
50%ANTH	0.04	0.05	-0.06	0.09
75%ANTH	0.06	0.02	-0.10	0.10
25%SILK	-0.07	0.14	-0.12	0.11
50%SILK	-0.05	0.12	-0.24	0.22
75%SILK	-0.11	0.13	-0.33	0.32
PSS	-0.11	0.10	-0.24	0.19
SI	-0.09	0.08	-0.33	0.30
SD	-0.14	0.12	-0.42	0.36

[1]Measured in one year only.

were lower than those correlations calculated at the same density. Evidently, errors associated with measurements of traits at low plant density are not the same as those associated with measurements at the high plant density. Therefore, selection at low density for improved high-density tolerance should not be biased by correlated errors.

Multiple Regression and Factor Analysis

Multiple regression models were fit using YIELD and BARREN as the dependent variables and the traits within each of the four groups (i.e., harvest, plant, flowering and canopy orientation) as the independent variables. This analysis was conducted to examine the effectiveness of the four groups of traits for predicting YIELD and BARREN and to determine the most effective traits within a group. Furthermore, this information supplemented that obtained from correlation analyses.

From the data in Table 34, it is evident that the groups of traits were not equally important for predicting YIELD and BARREN at the high plant density. Harvest traits displayed the largest R^2 values (0.83 and 0.79 for YIELD and BARREN, respectively) but flowering traits explained large percentages of the variability (i.e., 61 and 70% for YIELD and BARREN, respectively). Plant traits accounted for less than 25% and canopy-orientation traits explained only 3% of the variability for YIELD and BARREN. Similar values were observed at the low density (Table 35), except the R^2-values for flowering traits were only about one-half as large as they were at the high density (0.38 and 0.47 at 42,383 pl/ha and 0.61 and 0.70 at 96,875 pl/ha). Obviously, improvement of YIELD and

Table 34. Regression coefficients and coefficients of determination (R^2) from multiple regressions of yield and barrenness on several traits measured at 96,875 pl/ha

YIELD			BARREN		
Traits	b-value	R^2	Traits	b-value	R^2
BARREN	-0.51**	0.83	YIELD	-1.22**	0.79
GRNPLA	11.92**		GRNPLA	-1.25	
PTHT	-0.11	0.16	PTHT	0.44	0.24
ERHT	0.15		ERHT	-0.42	
ERHT:PTHT	0.10		ERHT:PTHT	-0.06	
TBN	-0.52**		TBN	0.65**	
PLA	-0.01*		PLA	0.01**	
LODG	0.19**		LODG	-0.32**	
LOV_j	0.46*	0.03	LOV_j	-0.56	0.03
LOV_a	-0.16		LOV_a	0.19	
LOV_b	-0.02		LOV_b	0.19	
25%ANTH	-2.14	0.61	25%ANTH	2.25	0.70
50%ANTH	2.63		50%ANTH	-1.83	
75%ANTH	-0.97		75%ANTH	0.28	
25%SILK	-4.67**		25%SILK	3.69	
50%SILK	1.06		50%SILK	0.48	
75%SILK	3.61*		75%SILK	-3.79	
PSS	-1.37		PSS	0.63	
SI	-5.21**		SI	6.30**	
SD	-0.70		SD	0.96	

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 35. Regression coefficients and coefficients of determination (R^2) from multiple regressions of yield and barrenness on several traits measured at 42,383 pl/ha

YIELD			BARREN		
Traits	b-value	R^2	Traits	b-value	R^2
PROLIF	0.39**	0.68	YIELD	-0.09	0.91
SECOND	-0.25		PROLIF	-0.87**	
GRNPLA	9.31**		SECOND	1.64**	
			GRNPLA	0.02	
PTHT	0.06	0.10	PTHT	-0.21	0.07
ERHT	0.09		ERHT	0.47	
ERHT:PTHT	18.85		ERHT:PTHT	-112.25	
TBN	-0.31*		TBN	0.24	
PLA	0.00		PLA	0.00	
LODG	0.03		LODG	-0.06	
LOV_j	0.00	0.09	LOV_j	0.00	0.07
LOV_a	-0.34*		LOV_a	0.28	
LOV_b	-0.10		LOV_b	0.30	
LOR_j	1.28		LOR_j	-3.60	
LOR_m	5.77**		LOR_m	-4.39**	
25%ANTH	-1.17	0.38	25%ANTH	0.79	0.47
50%ANTH	3.78		50%ANTH	0.65	
75%ANTH	-2.10*		75%ANTH	1.20	
25%SILK	1.00		25%SILK	0.21	
50%SILK	-2.07		50%SILK	-1.31	
75%SILK	0.19		75%SILK	-1.26	
PSS	3.15		PSS	0.37	
SI	-0.47		SI	2.25	
SD	3.58**		SD	3.48**	

*,** Significant at the 5% and 1% levels of probability, respectively.

BARREN by selecting for flowering traits would be most effective at the high plant density. Also, reducing barrenness by selecting for plant traits would be more effective at the high density (Table 34).

When traits were measured at the low density and used to predict YIELD and BARREN at the high density (Table 36), R^2-values for harvest and flowering traits were considerably lower than when these traits were measured at the high density (Table 36); but R^2-values for plant and canopy-orientation traits did not change. Therefore, improvement of high density yield potential in BSUL1 by selection for harvest and/or flowering traits should be greatest at high density, whereas, selection for plant and canopy-orientation traits should result in little improvement of high density yield potential because of the low associations between these traits with YIELD and BARREN at both densities.

All traits within each group did not make significant contributions to their respective models in determining the dependent variables YIELD and BARREN. For example, BARREN, GRNPLA and PROLIF (harvest); 25%SILK, 75%SILK, SI and SD (flowering); TBN, PLA and LODG (plant) and LOV_j, LOV_a and LOR_m (canopy orientation) traits appeared to be the most important within their respective groups in determining YIELD (Tables 34 and 35). Additionally, YIELD, PROLIF and SECOND (harvest); SI and SD (flowering); TBN, PLA and LODG (plant) and LOR_m (canopy orientation) appeared to be the most important within their respective groups in determining BARREN (Tables 34 and 35). When traits were measured at the low density and used to predict YIELD at the high density (Table 36), YIELD (harvest); SD (flowering); TBN (plant) and LOV_a and LOR_m (canopy orientation)

Table 36. Regression coefficients and coefficients of determination (R^2) from multiple regressions of yield and barrenness at 96,875 pl/ha on several traits measured at 42,383 pl/ha

YIELD			BARREN		
Traits	b-value	R^2	Traits	b-value	R^2
YIELD	0.86**	0.59	YIELD	-0.50**	0.52
BARREN	-0.03		BARREN	0.09	
PROLIF	0.11		PROLIF	-0.70*	
SECOND	0.23		SECOND	0.80	
GRNPLA	1.19		GRNPLA	-0.55	
PTHT	-0.41	0.13	PTHT	0.52	0.15
ERHT	0.84		ERHT	-0.75	
ERHT:PTHT	-89.77		ERHT:PTHT	55.39	
TBN	-0.62**		TBN	0.69**	
PLA	0.00		PLA	0.01*	
LODG	0.10		LODG	-0.23*	
LOV_j	-0.06	0.08	LOV_j	-0.05	0.08
LOV_a	-0.44*		LOV_a	0.42	
LOV_b	-0.17		LOV_b	0.64	
LOR_j	3.94		LOR_j	-8.37*	
LOR_m	6.79**		LOR_m	-7.52**	
25%ANTH	-0.31	0.40	25%ANTH	1.90	0.49
50%ANTH	-1.32		50%ANTH	5.81	
75%ANTH	-1.18		75%ANTH	1.81	
25%SILK	0.48		25%SILK	-1.30	
50%SILK	1.17		50%SILK	-7.36	
75%SILK	-0.04		75%SILK	1.23	
PSS	0.15		PSS	5.38	
SI	-0.43		SI	0.47	
SD	-4.08**		SD	4.96**	

contributed significantly to their respective models. When the same traits were used to predict BARREN at high density, YIELD and PROLIF (harvest); SD (flowering); TBN, PLA and LODG (plant) and LOR_j and LOR_m (canopy orientation) were the most important in their respective models.

I applied factor analysis to a correlation matrix of all traits so I could group the traits on the basis of common causative influences rather than according to the four arbitrary phenotypic classes (i.e., harvest, flowering, plant and canopy orientation). This technique is useful for explaining the intercorrelations among a set of selected variables, for ascertaining the number and nature of common causative influences, and for selecting a set of traits on the basis of the structural interrelationships among all traits studied.

Five common causative influences or factors were obtained by factor analysis of all traits measured at 96,875 pl/ha (Table 37). Collectively, these five factors accounted for 100% of the variance for all 23 traits. Communalities (the amount of variance of a variable accounted for by all factors collectively) ranged from 0.28 for TBN to 0.96 for 50%ANTH.

The relative importance of the factors is indicated by their order (Lee and Kaltsikes, 1973). Factor one included YIELD, BARREN, YIELDP, PROLIF, GRNPLA, TBN, 50%SILK, 75%SILK, PSS, SI and SD indicating that expressions of these 11 traits were influenced simultaneously by a common underlying force. The influence of a factor on a trait is determined by the square of the loading factor for that trait. Therefore, factor one accounted for 83% of the YIELD variance and 81% of the BARREN variance, at 96,875 pl/ha (Table 37). Factor two, on the other hand,

Table 37. Varimax-rotated factor matrix for yield, barrenness and 21 other traits of 144 S_1 families from BSUL1 grown at 96,875 pl/ha

Traits	Communalities	Factor loadings 1	2	3	4	5
Factor 1						
YIELD	0.86	0.91	-0.11	0.04	-0.02	-0.16
BARREN	0.87	-0.90	0.22	0.01	0.03	0.09
YIELDP	0.88	0.92	-0.11	0.05	-0.06	-0.13
PROLIF	0.87	0.90	-0.22	-0.01	-0.03	-0.09
GRNPLA	0.63	0.78	-0.04	0.07	-0.14	0.00
TBN	0.28	-0.36	0.07	0.14	-0.32	-0.16
50%SILK	0.94	-0.70	0.67	0.07	0.01	-0.05
75%SILK	0.93	-0.79	0.55	0.03	0.05	-0.05
PSS	0.83	-0.84	0.26	0.08	0.15	-0.14
SI	0.71	-0.81	0.20	-0.04	0.07	0.00
SD	0.83	-0.85	0.18	0.04	0.25	-0.14
Factor 2						
25%ANTH	0.93	-0.21	0.93	0.05	-0.14	0.07
50%ANTH	0.96	-0.22	0.93	0.04	-0.16	0.09
75%ANTH	0.93	-0.22	0.91	0.05	-0.21	0.11
25%SILK	0.88	-0.55	0.75	0.10	0.01	-0.08
Factor 3						
LOV_j	0.53	0.08	-0.21	0.68	-0.09	0.06
LOV_a	0.76	-0.05	0.19	0.84	0.09	-0.05
LOV_b	0.82	-0.02	0.18	0.88	-0.08	-0.05
Factor 4						
LODG	0.52	0.33	0.06	0.10	-0.63	0.09
ERHT	0.93	0.08	0.32	-0.03	-0.86	-0.30
ERHT:PTHT	0.70	0.16	0.03	0.00	-0.79	0.21
Factor 5						
PLA	0.66	-0.12	0.35	-0.05	-0.11	0.71
PTHT	0.76	-0.03	0.43	-0.04	-0.51	-0.56
Percentage of total variation	100.0	43.6	25.9	11.2	13.0	6.3

accounted for only 1% of the YIELD variance and 5% of the BARREN variance (Table 37).

Usually traits within each factor were highly correlated (Appendix Table 9). Therefore, measurements of one trait from each factor should be sufficient to preserve most of the information on all other traits in the factor. Fakorede, Smith and Mock (1978) suggested that selecting one trait with high loading from desirable factors may maximize grain yield more than indices based on traits selected from correlation and regression analyses.

Six factors were obtained with factor analysis of the 27 traits measured at 42,383 pl/ha (Table 38). Communalities ranged from 0.37 for SECOND to 0.97 for 50%ANTH. Tassel branch number (TBN) and flowering-duration traits with the exception of SI were of lesser importance at the low than at the high plant density; e.g., TBN, PSS and SD loaded in factor five rather than in factor one as they did at the high density. Factor one explained only 26.1% of the total variation at low density (Table 38) compared to 43.6% at the high density (Table 37). Days to flowering and canopy-orientation traits loaded in factors two and three, respectively, whereas, plant traits were distributed between the last three factors. When YIELD and BARREN measured at the high density were included in the model with the 27 traits measured at the low density, they loaded in factor one; and with the exception of TBN, all traits in this model loaded in the same six factors (Table 39). Communalities for the model ranged from 0.31 for SECOND to 0.97 for 50%ANTH.

Table 38. Varimax-rotated factor matrix for yield, barrenness and 24 other traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha

Traits	Communalities	Factor loadings 1	2	3	4	5	6
Factor 1							
YIELD	0.88	0.89	-0.19	0.06	-0.13	-0.02	0.16
BARREN	0.80	-0.85	0.09	0.02	-0.01	0.18	0.17
YIELDP	0.88	0.90	-0.18	0.07	-0.14	-0.01	0.10
PROLIF	0.83	0.88	-0.07	-0.01	-0.08	-0.20	-0.02
SECOND	0.37	0.46	-0.02	0.01	-0.25	-0.14	0.27
GRNPLA	0.58	0.66	-0.15	-0.01	-0.35	0.02	-0.04
SI	0.63	-0.64	0.10	0.01	-0.02	0.41	0.21
Factor 2							
25%ANTH	0.95	-0.06	0.95	0.05	-0.18	-0.01	0.07
50%ANTH	0.97	-0.08	0.96	0.07	-0.18	0.01	0.07
75%ANTH	0.94	-0.12	0.94	0.07	-0.17	0.04	0.02
25%SILK	0.95	-0.21	0.87	0.02	-0.04	0.36	0.09
50%SILK	0.97	-0.28	0.83	0.05	-0.05	0.44	0.09
75%SILK	0.93	-0.46	0.69	0.02	-0.04	0.46	0.17
Factor 3							
LOV_j	0.46	-0.01	-0.04	0.65	0.00	-0.08	-0.17
LOV_a	0.73	-0.06	0.12	0.83	-0.05	0.10	0.11
LOV_b	0.79	-0.08	0.06	0.88	-0.07	-0.02	0.05
LOR_j	0.58	0.07	-0.04	0.72	-0.04	0.06	-0.21
LOR_m	0.71	0.15	0.12	0.79	0.00	0.04	0.20
Factor 4							
LODG	0.48	0.06	0.00	0.18	-0.61	-0.26	0.07
PTHT	0.60	0.15	0.25	-0.01	-0.67	0.26	0.02
ERHT	0.93	0.19	0.22	-0.02	-0.92	0.09	-0.02
ERHT:PTHT	0.60	0.15	0.13	0.01	-0.73	-0.14	-0.06
Factor 5							
TBN	0.51	-0.01	0.15	0.08	-0.04	0.61	-0.34
PSS	0.85	-0.38	0.29	0.01	0.13	0.77	0.08
SD	0.58	-0.55	0.22	-0.01	0.16	0.72	0.15
Factor 6							
PLA	0.68	0.00	0.24	-0.04	0.01	-0.02	0.78
Percentage of total variation	100.0	26.1	26.3	15.9	13.2	12.7	5.8

Table 39. Varimax-rotated factor matrix for yield and barrenness of 144 S_1 families grown at 96,875 pl/ha (HI) and several other traits of these families grown at 42,383 pl/ha

Traits	Communalities	Factor loadings 1	2	3	4	5	6
Factor 1							
YIELD (HI)	0.75	0.79	-0.31	0.06	-0.04	-0.11	0.13
BARREN (HI)	0.71	-0.73	0.35	-0.03	-0.01	0.21	0.01
YIELD	0.89	0.90	-0.16	0.05	-0.15	0.03	0.14
YIELDP	0.88	0.91	-0.15	0.06	-0.15	0.02	0.08
SECOND	0.31	0.47	0.03	0.01	-0.23	-0.12	0.15
PROLIF	0.83	0.87	-0.03	-0.01	-0.07	-0.24	-0.08
BARREN	0.78	-0.83	0.07	0.04	-0.01	0.24	0.18
GRNPLA	0.57	0.65	-0.14	-0.02	-0.36	0.02	-0.05
SI	0.64	-0.61	0.09	0.02	-0.03	0.47	0.18
Factor 2							
25%ANTH	0.95	-0.09	0.94	0.06	-0.19	-0.03	0.08
50%ANTH	0.97	-0.12	0.95	0.07	-0.18	0.00	0.08
75%ANTH	0.93	-0.15	0.93	0.07	-0.17	0.02	0.03
25%SILK	0.95	-0.24	0.88	0.02	-0.04	0.34	0.01
50%SILK	0.96	-0.30	0.83	0.06	-0.05	0.43	0.00
75%SILK	0.93	-0.47	0.69	0.02	-0.05	0.48	0.10
Factor 3							
LOV_j	0.46	-0.02	-0.05	0.65	0.00	-0.12	-0.14
LOV_a	0.72	-0.05	0.13	0.83	-0.04	0.10	0.05
LOV_b	0.79	-0.07	0.05	0.88	-0.07	-0.01	0.06
LOR_j	0.57	0.07	-0.04	0.72	-0.03	0.02	-0.20
LOR_m	0.71	0.17	0.13	0.79	0.00	0.08	0.18
Factor 4							
PTHT	0.62	0.12	0.24	-0.01	-0.69	0.26	0.02
ERHT	0.94	0.18	0.22	-0.02	-0.92	0.06	-0.05
ERHT:PTHT	0.60	0.16	0.15	0.01	-0.71	-0.19	-0.11
LODG	0.47	0.08	-0.01	0.18	-0.60	-0.24	0.12
Factor 5							
PSS	0.84	-0.37	0.30	0.02	0.13	0.77	-0.09
SD	0.92	-0.54	0.22	-0.01	0.16	0.74	0.01
Factor 6							
TBN	0.59	-0.06	0.19	0.08	-0.04	0.45	-0.58
PLA	0.56	0.01	0.28	-0.04	0.00	0.11	0.69
Percentage of total variation	100.0	29.9	25.6	14.9	12.4	11.9	5.3

Four general conclusions were drawn from my factor analyses: 1) Harvest traits always loaded in factor one and explained a major portion of the total variation, 2) with the exception of SI, flowering-duration traits were more important at high than at low plant density, 3) TBN, ERHT and PLA usually loaded in different factors indicating that these plant traits were not of equal importance and should not be considered as one group for selection purposes, 4) harvest and flowering traits (i.e., factors one and two) explained 70 and 52% of the total variation at high and low densities, respectively.

Stepwise multiple regression analysis indicated that PROLIF, GRNPLA, PTHT, 25%SILK, LODG and 50%ANTH were important in predicting grain yield at the high plant density (Table 40). PROLIF and GRNPLA accounted for 80% of the variation for grain yield. When all 23 traits were included in the analysis, only 84% of the variance for YIELD was explained. At the low density (Table 41), PROLIF and GRNPLA were also the most important traits, and they accounted for 65% of the variance for YIELD. These traits, plus LOR_m, BARREN, 25%ANTH, PTHT and PLA explained 72% of the variation for grain yield. All 26 traits measured at the low density accounted for only 73% of the variation for grain yield. Grain yield (YIELD), 75%SILK, SECOND, TBN and PTHT (all measured at the low density) accounted for 65% of the variation for YIELD at the high density (Table 42). When all 27 low-density traits were included in the analysis only 69% of the variance for high-density YIELD was explained.

Percent barrenness (BARREN) at the high density was predicted most effectively by YIELDP, SI and 25%SILK (Table 43). These three traits

Table 40. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield on several traits measured at 96,875 pl/ha

No. of traits in model	PROLIF	GRNPLA	PTHT	25%SILK	50%SILK	LODG	50%ANTH	LOV_j	R^2
1	0.63**								0.77
2	0.52**	9.67**							0.80
3	0.54**	8.93**	0.08*						0.81
4	0.51**	8.20**	0.10**	-0.35*					0.81
5	0.55**	8.56**	0.10**	-0.95**	0.58				0.82
6	0.52**	7.84**	0.11**	-0.79**	-[a]	-0.64*	0.72*		0.82
7	0.52**	7.60**	0.11**	-0.82**	-	-0.07*	0.78*	0.15	0.83

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 41. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield on several traits measured at 42,383 pl/ha

No. of traits in model	PROLIF	GRNPLA	LOR_m	BARREN	25%ANTH	PTHT	PLA	TBN	R^2
1	0.50**								0.53
2	0.35**	9.69**							0.65
3	0.35**	9.74**	1.77**						0.67
4	0.21**	9.35**	1.81**	-0.20*					0.68
5	0.34**	8.84**	2.02**	-[a]	-0.63*	0.07*			0.69
6	0.34**	8.94**	1.98**	-	-0.74**	0.08**	0.00*		0.70
7	0.22	8.61**	1.97**	-0.19*	-0.68**	0.08**	0.00*		0.72
8	0.21**	8.58**	2.02**	-0.19*	-0.65**	0.08**	0.00*	-0.13	0.72

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 42. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield at 96,875 pl/ha on several traits measured at 42,383 pl/ha

No. of traits in model	YIELD	75%SILK	SECOND	TBN	PTHT	PLA	LOR_m	LOV_b	R^2
1	1.04**								0.56
2	0.84**	-0.85**							0.62
3	0.79**	-0.84**	0.42						0.63
4	0.87**	-0.77*	0.40*	0.24*					0.64
5	0.87**	-0.64**	0.41*	-0.23*	-0.08				0.65
6	0.89**	-0.56**	0.43*	-0.24*	-0.08	0.00			0.66
7	0.87**	-0.59**	0.43*	-0.25*	-0.08	0.00	1.25		0.66
8	0.86**	-0.58**	0.43*	-0.26*	-0.09	0.00	1.99	-0.11	0.66

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 43. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness on several traits measured at 96,875 pl/ha

No. of traits in model	YIELDP	SI	25%SILK	LOV_j	50%SILK	PTHT	50%ANTH	ERHT	YIELD	R^2
1	-1.13**									0.79
2	-0.84**	1.67**								0.84
3	-0.81**	1.57**	0.83**							0.85
4	-0.82**	1.58**	0.86**	0.20						0.85
5	-0.81**	1.32**	-[a]	0.19	0.47**	0.08*				0.86
6	-0.83**	1.46**	-	0.21*	-	0.14*	0.74**	-0.14		0.86
7	-0.56**	1.46**	-	0.20	-	0.16*	0.71**	-0.17	-0.31	0.86

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

explained 85% of the variation for BARREN compared to only 87% when all 21 traits were included in the model. Yield per plant (YIELDP), SI, SD and SECOND accounted for 63% of the variation for BARREN at the low density (Table 44) and all 22 traits explained only 65%. The traits, PROLIF, 75%SILK, YIELD, SECOND and PTHT were the most effective low-density traits for predicting BARREN at the high density (i.e., they accounted for 61% of the variation, Table 45). All 27 low-density traits explained 68% of the variation of BARREN at the high density.

Traits are included in the regression model according to their relative importance in determining the dependent variable; i.e., either YIELD or BARREN. My data (Tables 40-45) indicated that the best multiple linear regression equation for predicting YIELD or BARREN at either the low or high plant density should include no more than three traits since the increase in R^2-values beyond inclusion of that number of traits usually was less than 1% per additional trait.

Stepwise multiple regression (to develop models with the greatest R^2-values) was performed using all traits (except harvest) as the independent variables to determine how accurately YIELD and BARREN could be predicted without using harvest traits. At the high density (Table 46), 75%SILK, 50%ANTH, PTHT, 25%ANTH, 25%SILK and SI accounted for most of the variation in YIELD; and at the low density (Table 47), SD, PTHT, SI, 75%ANTH, 75%SILK and LOR_m were most important. Traits measured at the high density, however, explained approximately 20% more variation in YIELD than traits measured at the low density. When low-density traits were used to explain the variation for YIELD at the high density, a

Table 44. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness on several traits measured at 42,383 pl/ha

No. of traits in model	YIELDP	SI	SD	SECOND	TBN	PTHT	LOV_j	PLA	R^2
1	-0.39**								0.53
2	-0.30**	1.49**							0.61
3	-0.27**	1.13**	0.75*						0.62
4	-0.28**	1.12**	0.82*	0.26					0.63
5	-0.28**	1.09**	0.96**	0.27	-0.12				0.63
6	-0.29**	1.06**	0.94**	0.25	-0.13	0.04			0.64
7	-0.29**	1.04**	0.97**	0.26	-0.14	0.04	0.10		0.64
8	-0.29**	1.04**	0.92*	0.24	-0.13	0.04	0.10	0.00	0.64

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 45. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness at 96,875 pl/ha on several traits measured at 42,383 pl/ha

No. of traits in model	PROLIF	75%SILK	YIELD	SECOND	PTHT	LODG	25%ANTH	YIELDP	R^2
1	-0.89**								0.46
2	-0.60**	1.75**							0.59
3	-0.44**	1.64**	-0.36*						0.60
4	-0.55**	1.58**	-0.33*	0.57					0.61
5	-0.42**	1.44**	-0.44**	0.56	0.13				0.62
6	-0.40**	1.41**	-0.50**	0.55	0.12*	-0.12			0.62
7	-0.57**	0.91*	-0.47**	0.58	0.13	-0.14*	0.96		0.64
8	-0.62**	0.85*	-1.24*	0.66	0.13	-0.14*	1.10	0.38	0.64

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 46. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield on several traits measured at 96,875 pl/ha

No. of traits in model	75%SILK	50%ANTH	PTHT	25%ANTH	LOV_b	PSS	25%SILK	SI	75%ANTH	R^2
1	-1.61**									0.53
2	-2.01**	1.40**								0.57
3	-1.99**	1.09**	0.12*							0.58
4	-2.01**	3.24*	0.13*	-2.22						0.59
5	-2.00**	3.31**	0.13*	-2.37	0.12					0.60
6	-1.70**	3.02*	0.12*	-2.33	0.13	-0.52				0.60
7	-3.29**	3.33**	0.13**	-2.40	0.12	-[a]	-5.21**	-5.32**		0.62
8	-3.40**	4.47**	0.14**	-2.54*	0.13	-	-5.33**	-5.41**	-1.00	0.63

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 47. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield on several traits measured at 42,383 pl/ha

No. of traits in model	SD	PTHT	SI	75%ANTH	25%SILK	LOR_m	25%ANTH	PLA	LOV_a	R^2
1	-2.37**									0.30
2	-2.39**	0.12**								0.34
3	-1.62**	0.13**	-1.05**							0.38
4	-3.20**	0.16**	-[a]	-2.35**	1.74**					0.41
5	-3.14**	0.15**	-	-2.45**	1.74**	2.53**				0.44
6	-3.61**	0.16**	-	-1.86**	2.47**	2.70**	-1.45			0.46
7	-3.58**	0.16**	-	-1.86**	2.37**	2.65**	-1.46	0.00		0.47
8	-3.50**	0.16**	-	-1.83**	2.34**	3.85**	-1.41	0.00	-0.14	0.48

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

model composed of 75%SILK, SD, LOR_m, ERHT, TBN, SI and LOV_a resulted in an R^2-value of 0.45 (Table 48). Therefore, by excluding harvest traits from the regression models, explanation of the variation for YIELD was approximately 76, 67 and 68% as efficient as models including these traits for high density, low density and across densities, respectively.

Days from July 1 to 75% silk emergence (75%SILK), 50%SILK, SI, SD, PSS and ERHT:PTHT were the most important traits explaining the variation for BARREN at 96,875 pl/ha (Table 49). In fact, most of the variation in BARREN was explained by 75%SILK exclusively (i.e., R^2 = 0.65), and 75%SILK, 50%SILK and SI were associated with an R^2-value of 0.69. Silking interval (SI) and SD explained most of the variation for BARREN at 42,383 pl/ha (i.e., R^2 = 0.45, Table 50). Similar to predictions for YIELD, traits measured at the high density explained approximately 20% more variation for BARREN than traits measured at the low density. The trait, 75%SILK, measured at the low density accounted for 44% of the variation for BARREN at the high density (Table 51). The best model (using low-density traits to predict high-density BARREN) included ERHT:PTHT, LOR_m, SI, LOV_a, SD and 25%ANTH and resulted in an R^2-value of 0.50 (Table 51). By excluding harvest traits from the regression models, explanation of the variation for BARREN, therefore, was approximately 81, 77 and 78% as efficient as models including these traits for high density, low density and across densities, respectively.

The traits I measured usually accounted for more of the variation for BARREN than for YIELD, and R^2-values were about 20% lower at the low density. In all models, one to four traits accounted for most of the variation for the dependent variable. Multiple linear regression

Table 48. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of yield at 96,875 pl/ha on several traits measured at 42,383 pl/ha

No. of traits in model	75%SILK	SD	LOR_m	ERHT	TBN	SI	LOV_a	50% SILK	R^2
1	-1.74**								0.34
2	-1.04**	-1.82**							0.38
3	-1.13**	-1.66**	3.14**						0.41
4	-1.32**	-1.27*	3.14**	0.14					0.42
5	-1.34**	-1.02	3.27**	0.16	-0.25				0.43
6	-1.96**	-1.55**	3.55**	0.17	-0.26	-0.96*			0.44
7	-1.93**	-1.53**	5.07**	0.17	-0.23	-0.92*	-0.18		0.45
8	-[1]	-2.90**	4.96**	0.16	-0.26	-1.42	-0.18	1.07	0.45

[1]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 49. Partial correlation coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness on several traits measured at 96,875 pl/ha

No. of traits in model	75%SILK	50%SILK	SI	SD	ERHT:PTHT	25%ANTH	PSS	PLA	50%ANTH	R^2
1	2.48**									0.65
2	-[a]	1.37**	2.82**							0.69
3	-	1.11**	2.44**	0.95						0.69
4	-	1.20**	2.43**	0.74	-0.28					0.70
5	-	-	2.49**	0.71	-0.26	1.24**	1.22**			0.70
6	-	-	2.46**	0.74	-0.27	1.18**	1.22*	0.00		0.70
7	-	1.26*	2.52**	0.64	-0.26	2.21	-	0.00	-2.30	0.70

[a]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 50. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness on several traits measured at 42,383 pl/ha

No. of traits in model	SI	SD	TBN	75%ANTH	75%SILK	PTHT	25%ANTH	LOR_m	LOV_a	R^2
1	2.75**									0.38
2	1.70**	1.72**								0.45
3	1.65**	1.88**	-0.15							0.46
4	2.18**	2.54**	-[1]	1.14	-0.97					0.46
5	2.17**	2.81**	-0.18	1.29	-1.07					0.47
6	2.14**	2.71**	-0.17	1.34	-1.01	-0.05				0.48
7	2.41**	3.06**	-0.17	1.07	1.43	-0.05	0.78			0.48
8	2.14**	2.73**	-0.19	1.41	-1.08	-0.04	-	-2.20	0.16	0.49

[1]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 51. Partial regression coefficients and coefficients of determination (R^2) from stepwise multiple regressions of barrenness at 96,875 pl/ha and several traits measured at 42,383 pl/ha

No. of traits in model	75%SILK	ERHT:PTHT	LOR_m	SI	LOV_a	SD	25%ANTH	LOV_j	R^2
1	2.74**								0.44
2	2.73**	-61.43*							0.46
3	2.76**	-60.16*	-3.22*						0.48
4	2.42**	-53.72*	-3.03	0.88					0.48
5	2.37**	-55.61*	-4.79*	0.85	0.21				0.49
6	-[1]	-46.89**	-5.00*	1.94**	0.20	2.63**	2.63**		0.50
7	-	-47.17	-5.31*	1.92**	0.17	2.69	2.51**	0.17	0.50

[1]Trait does not enter into model.

*,**Significant at the 5% and 1% levels of probability, respectively.

equations to maximize YIELD and minimize BARREN are presented in Table 52. Evidently, from these analyses, the best traits for maximizing R^2-values for YIELD and BARREN are different at each density. At 96,875 pl/ha, 75%SILK, 50%ANTH and PTHT were the most important traits for explaining the variation for YIELD; whereas, at 42,383 pl/ha, SD, PTHT, 75%ANTH, 25%SILK and LOR_m accounted for most of the variation for YIELD. Most of the variation for BARREN at the high density was explained by 75%SILK, 50%SILK and SI; whereas, SI and SD accounted for most of the variation for BARREN at the low plant density. When low-density traits were used to explain the variation in YIELD and BARREN at the high density, 75%SILK and LOR_m appeared in each model (Table 52). Additionally, SD and ERHT:PTHT (measured at the low density) were important in explaining the variance for YIELD and BARREN, respectively, at the high density. Inclusion of these traits in a selection index, therefore, should result in reduced barrenness and improved yield potential of BSUL1 when it is grown at a high plant density.

Variability for Net Photosynthesis and Its Relationship with Grain Yield

High photosynthetic capacity has been considered a requisite trait for an efficient maize ideotype (Mock and Pearce, 1975). If high photosynthetic capacity is to be incorporated into an ideotype, adequate genetic variability for photosynthesis must exist in maize breeding populations.

Large differences in CER among the 64 random S_1 families I evaluated were observed all three years (Table 53). Combined over 1975 and 1976,

Table 52. Multiple linear regression equations for predicting YIELD and BARREN at 96,875 pl/ha (HI) and 42,383 pl/ha (LO)

Regression equation			R^2
YIELD(HI)[a]	=	-1.99 75%SILK + 1.09 50%ANTH + 0.12 PTHT	0.58
YIELD(LO)[b]	=	-3.14 SD + 0.15 PTHT - 2.45 75%ANTH + 1.74 25%SILK + 2.53 LOR_m	0.44
BARREN(HI)[a]	=	-1.37 50%SILK - 2.82 SI	0.69
BARREN(LO)[b]	=	-1.70 SI - 1.72 SD	0.45
YIELD(HI)[b]	=	-1.13 75%SILK - 1.66 SD + 3.14 LOR_m	0.41
BARREN(HI)[b]	=	-2.73 75%SILK + 60.16 ERHT:PTHT + 3.22 LOR_m	0.48

[a]Independent variables measured at high density.

[b]Independent variables measured at low density.

Table 53. Variation for CO_2 exchange rate (mg $CO_2/dm^2/hr$) among 64 random S_1 families from BSUL1

	1974	1975	1976	Combined[a]
Range	14.1 - 50.4	15.0 - 39.8	15.0 - 38.2	15.0 - 38.8
$\bar{x}$	28.1	28.3	26.6	27.7
L.S.D. (0.05)	15.6	8.5	10.3	8.4
C.V. (%)	27.7	15.1	19.4	17.2

[a]Combined over 1975 and 1976.

CER ranged from 15.0 to 38.8 mg $CO_2/dm^2/hr$, specific leaf weight ranged from 5.0 to 6.3 mg/cm^2 (Table 54), and leaf thickness ranged from 181.4 to 244.6 μ (Table 55). These values are similar to those reported by Crosbie (1977) for 64 random inbred lines from Iowa Stiff Stalk Synthetic (BSSS) maize population.

Genotypic differences for all three traits were highly significant (Table 56), but genotype x environment interaction (G x E) was significant for CER only. The genotype x environment variance component for CER (6.39±3.46), however, was not significantly different from zero (Table 57). Estimates of genotypic variances were 1.2, 5.0 and 6.6 times larger than estimates of G x E variances for CER, SLW and LT, respectively.

Heritability estimates were 0.47 for CER, 0.68 for SLW and 0.75 for LT (Table 57), indicating that genotypic variation in BSUL1 was sufficient to permit selection for improvement of the three traits. Genotypic correlations (Table 58), however, indicated that none of the three traits explained more than 5% of the variation for grain yield. Obviously, CER, SLW and LT were not the primary factors limiting grain yield in BSUL1. Consequently, selection for improved CO_2 exchange rates *per se* in the population would not be associated with an increase in grain yield.

Table 54. Variation for specific leaf weight (mg/cm^2) among 64 random S_1 families from BSUL1

	1974	1975	1976	Combined[a]
Range	5.3 - 7.3	5.1 - 6.3	4.8 - 6.5	5.0 - 6.3
$\bar{x}$	6.1	5.7	5.7	5.7
L.S.D. (0.05)	0.8	0.7	0.6	0.4
C.V. (%)	6.2	6.3	4.9	5.7

[a]Combined over 1975 and 1976.

Table 55. Variation for leaf thickness (micrometers) among 64 random S_1 families from BSUL1

	1974	1975	1976	Combined[a]
Range	189.2 - 263.4	211.6 - 273.6	159.3 - 220.0	181.4 - 244.6
$\bar{x}$	221.5	241.8	188.7	215.4
L.S.D. (0.05)	30.5	23.6	22.9	18.5
C.V. (%)	7.0	4.9	6.0	5.4

[a]Combined over 1975 and 1976.

Table 56. Mean squares from analyses of variance for CO_2 exchange rate (CER), specific leaf weight (SLW) and leaf thickness (LT) combined over 1975 and 1976

Source	df	Mean squares		
		CER	SLW	LT
Environments (E)	1	187.5	0.02	180737.44**
Replicates/E	2	355.2	0.15	7.26
Genotypes (G)	63	66.3**	0.30**	679.55**
G x E	63	35.2*	0.10	172.65
Pooled error				
Randomized block	126	29.9	0.11	139.10
Effective	98	22.4	0.10	134.19

*,**Significant at the 5% and 1% levels of probability, respectively.

Table 57. Variance components and heritability estimates from combined analyses for CO_2 exchange rate (CER), specific leaf weight (SLW) and leaf thickness (LT) of 64 random S_1 families from $BSUL_1$

	CER		SLW		LT	
Component	Estimate	S.E.[a]	Estimate	S.E.	Estimate	S.E.
V_g[b]	7.80	3.29	0.05	0.01	126.73	30.74
V_{ge}[c]	6.39	3.46	0.00	0.01	19.23	17.82
h^2	0.47	0.13	0.68	0.04	0.75	0.03

[a]S.E. = standard error.

[b]V_g = genotypic variance.

[c]V_{ge} = genotype x environment variance.

Table 58. Phenotypic (r_{ph}), genotypic (r_g) and error (r_e) correlations among CO_2 exchange rate (CER), specific leaf weight (SLW), leaf thickness (LT), YIELD at 42,383 pl/ha (LO) and YIELD at 96,875 pl/ha (HI) of 64 random S_1 families from BSUL1

		SLW	LT	YIELD(LO)	YIELD(HI)
CER	r_{ph}	0.09	0.12	0.05	0.00
	r_g	0.30	0.25	0.22	0.05
	r_e	0.02	0.12	-0.01	0.02
SLW			0.54**	0.07	-0.04
			0.53	-0.01	-0.10
			0.53	0.03	-0.02
LT				-0.07	-0.09
				-0.19	-0.17
				0.02	0.06
YIELD(LO)					0.77**
					1.02
					0.15

**Significant at the 1% level of probability.

Selection

Single-trait selection

Success in plant breeding depends on selection advance. Table 59 presents the expected gains (ΔG_i) from single-trait selection of various traits at two plant densities using a 10% selection intensity (i.e., $k = 1.75$).

Most traits at both densities exhibited high predicted gains from direct selection. Gains (expressed as percentages of the mean) for 16 of the 23 traits common to each density were greater at the high than the low density. Expected improvement for YIELD at the high density was twice that for YIELD at the low density, and predicted gains for PROLIF and GRNPLA at the high density were three times larger than those expected for the same traits at the low density.

Predicted gains for LOV's were similar across densities (Table 59), suggesting that improvement of these traits through selection would be equal at either density. However, selection for LOR's (which are easier to evaluate than LOV's), would result in twice the improvement in canopy orientation than selection for LOV's (i.e., for LOR_m improvement would be 27.6% of the mean and for LOV_a and LOV_b it would be 18.7 and 14.4%, respectively).

As discussed previously, unfavorable flowering-duration traits and resultant barrenness limited grain yields of BSUL1 at 96,875 pl/ha. Selection for decreased flowering duration at that density would result in 62.5, 50.6 and 40.8% improvements (relative to the population means) in PSS, SD and SI, respectively. Predicted gains for these traits (expressed

Table 59. Predicted gains from single-trait selection (ΔG_i) among 144 S_1 families from BSUL1 (10% selection intensity)

	96,875 pl/ha			42,383 pl/ha		
Traits	Population means	ΔG_i	% of population mean	Population means	ΔG_i	% of population mean
YIELD	38.3	13.9	36.2	43.5	7.3	16.9
BARREN	35.5	-20.7	58.2	13.2	-6.8	51.6
YIELDP	42.7	15.0	35.2	93.0	14.3	15.4
PROLIF	64.8	20.8	32.1	91.2	10.7	11.7
SECOND	-[1]	-	-	1.9	2.3	122.4
GRNPLA	1.0	0.14	14.0	1.9	0.08	4.4
25%ANTH	22.7	-3.4	15.0	21.9	-3.2	14.4
50%ANTH	24.7	-3.4	13.8	23.7	-3.3	13.7
75%ANTH	26.4	-3.4	13.0	25.3	-3.3	13.0
25%SILK	26.8	-4.4	16.4	24.5	-4.1	16.7
50%SILK	30.3	-6.1	20.0	26.9	-4.5	16.6
75%SILK	34.3	-7.2	20.9	29.9	-5.2	17.4
PSS	5.5	-3.4	62.5	3.2	-1.8	57.1
SI	7.5	-3.1	40.8	5.5	-1.9	34.9
SD	6.4	-3.2	50.6	3.9	-2.5	64.6
LOV_j	56.7	4.5	7.9	51.6	2.7	5.3
LOV_a	50.6	9.7	19.1	50.9	9.5	18.7
LOV_b	48.1	7.8	16.3	48.3	6.9	14.4
LOR_j	-	-	-	1.5	0.46	30.6
LOR_m	-	-	-	2.1	0.58	27.6
PTHT	162.9	-17.9	11.0	161.1	-19.5	12.1
ERHT	76.8	11.6	15.1	72.7	12.7	17.5
ERHT:PTHT	0.46	0.04	8.7	0.44	0.04	10.2
TBN	16.2	-6.5	39.9	16.5	-7.47	45.3
PLA	5327	-317.5	6.0	5585	-280.9	5.0
LODG	20.8	-19.3	92.7	14.6	-11.4	77.9
CER	-	-	-	27.5	3.3	12.2
SLW	-	-	-	5.7	-0.33	5.7
LT	-	-	-	215.0	-17.1	8.0

[1]Trait not measured.

as a percentage of the population mean) were similar at 42,383 pl/ha (Table 59). Actual gains (ΔG_i) at this density, however, were only half those observed at 96,875 pl/ha.

Expected gains for yield and barrenness associated with selection for several other traits were examined to determine whether more progress could be achieved via indirect selection for a correlated trait than by direct selection for a primary trait. Indirect selection would be better than direct selection if the correlated trait had a substantially higher heritability than the primary trait and the genetic correlation between the two was high; or, if a substantially higher intensity of selection could be applied to the correlated trait than to the primary trait.

Expected gains for YIELD (ΔG_y) and BARREN (ΔG_b) observed with selection for various traits measured at 96,875 pl/ha are presented in Table 60. Indirect selection resulted in greater improvement for BARREN than YIELD when selection was practiced for 21 of the 23 traits; but, with the exception of GRNPLA, correlated responses for each trait were smaller than the responses from direct selection. Selection for increased GRNPLA resulted in a 79.3% reduction in BARREN relative to the population mean. Selection for decreased 75%SILK, PSS and SI resulted in reductions in BARREN of 52.3, 49.4 and 49.3%, respectively. Barrenness was reduced by 16.3, 13.8 and 13.7% (relative to the population mean) by selection for reduced TBN, PTHT and PLA, respectively. Increases in YIELD ranged from 60.8% through selection for higher GRNPLA to 1.4% through selection for improved LOV_b.

Obviously, the high density yield potential of BSUL1 could be

Table 60. Predicted gains from selection for yield (ΔG_y) and reduced barrenness (ΔG_b) when selection was based on several traits of 144 S_1 families from BSUL1 grown at 96,875 pl/ha (10% selection intensity)

	YIELD		BARREN	
96,875 pl/ha	ΔG_y	% of population mean	ΔG_b	% of population mean
YIELD	13.9	36.2	-18.0	50.7
BARREN	13.0	33.8	-20.7	58.2
YIELDP	13.3	34.6	-17.9	50.4
PROLIF	9.9	25.8	-17.1	48.0
GRNPLA	23.3	60.8	-28.1	79.3
25%ANTH	6.1	16.0	-10.6	29.9
50%ANTH	5.6	14.6	-10.4	29.3
75%ANTH	6.4	16.8	-11.3	31.7
25%SILK	9.8	25.2	-14.5	40.9
50%SILK	11.1	28.9	-17.4	49.0
75%SILK	11.9	31.0	-18.6	52.3
PSS	11.9	31.0	-17.5	49.4
SI	10.7	28.0	-17.5	49.3
SD	11.4	29.9	-16.4	46.3
LOV_j	1.7	4.5	-0.5	1.4
LOV_a	-1.1	3.0	3.0	8.4
LOV_b	-0.5	1.4	1.8	5.1
PTHT	-1.4	3.7	-4.9	13.8
ERHT	-1.9	4.8	0.5	1.4
ERHT:PTHT	4.2	10.9	-5.7	16.2
TBN	4.1	10.8	-5.8	16.3
PLA	1.1	2.9	-4.9	13.7
LODG	-6.1	15.8	7.1	20.0

improved by indirect selection. Since improvement for BARREN was greater than that for YIELD *per se*, the most efficient selection program initially would involve enhancement of yield potential through improvement of the traits that cause the greatest reduction in barrenness and are relatively simple to measure (i.e., 75%SILK, PSS, SI and TBN). Since selection for these traits is rapid and inexpensive, and since they displayed lower G x E variance components than YIELD and BARREN (Tables 15 through 18), effective selection for reduced barrenness and increased yield potential may be conducted in one environment. After a few cycles of selection for these traits (possibly when BSUL1 has the ability to produce at least one ear per plant consistently at high densities), selection for yield *per se* could be initiated for continued population improvement.

Expected gains for YIELD and BARREN at both densities associated with selection for several traits at the low density are presented in Table 61. Indirect selection produced more consistent and greater decreases in BARREN than increases in YIELD. Predicted decreases in BARREN at the low density ranged from 58.3% through selection for decreased SD to 0.9% through selection for improved LOR_j; whereas, expected decreases in BARREN at the high density ranged from 58.8% through selection for increased GRNPLA to 1.3% through increased LOR_j.

With the exception of GRNPLA, correlated responses for YIELD at the low density were smaller than gains from selection for YIELD *per se* (Table 61). Selection for increased PROLIF and GRNPLA and for reduced 75%SILK and SD resulted in greater reduction of BARREN than selection for BARREN *per se* (Table 61). Selection for traits at the low density

Table 61. Predicted gains from selection for yield (ΔG_y) and reduced barrenness (ΔG_b) when selection was based on several traits of 144 S_1 families from BSUL1 grown at 42,383 pl/ha (10% selection intensity)

	42,383 pl/ha				96,875 pl/ha			
	YIELD		BARREN		YIELD		BARREN	
42,383 pl/ha	ΔG_y	% of pop. mean	ΔG_b	% of pop. mean	ΔG_y	% of pop. mean	ΔG_b	% of pop. mean
YIELD	7.3	16.9	-6.5	49.1	11.5	30.0	-13.7	38.5
BARREN	5.8	13.3	-6.8	51.6	10.1	26.3	-15.1	42.6
YIELDP	7.1	16.3	-6.3	48.0	10.8	28.1	-13.0	36.5
PROLIF	6.4	14.7	-7.1	54.1	10.5	27.4	-14.1	39.7
SECOND	4.3	10.0	-3.4	26.0	5.8	15.1	-6.9	19.4
GRNPLA	13.9	31.9	-7.6	57.2	17.7	46.2	-20.9	58.8
25%ANTH	1.7	3.9	-2.3	17.7	6.3	16.4	-10.6	29.8
50%ANTH	1.9	4.4	-2.6	19.6	6.9	18.0	-11.1	31.2
75%ANTH	2.7	6.2	-3.2	23.9	6.7	17.4	-11.6	32.7
25%SILK	4.1	9.3	-5.0	37.9	9.6	25.0	-14.1	39.7
50%SILK	4.7	10.8	-5.3	39.9	12.2	31.9	-14.8	41.5
75%SILK	5.9	13.5	-6.9	52.3	11.4	29.8	-16.9	47.7
PSS	5.9	13.5	-5.9	44.6	9.5	27.7	-12.7	35.9
SI	6.0	13.7	-6.6	49.9	11.1	28.8	-13.6	38.3
SD	6.8	15.6	-7.7	58.3	10.6	27.7	-14.6	41.1
LOV_j	2.4	5.4	-1.3	9.4	3.1	8.0	-3.4	9.5
LOV_a	-1.5	3.5	2.6	19.9	-2.0	5.1	2.8	7.8
LOV_b	1.9	4.5	0.9	6.5	-2.0	5.1	1.6	4.4
LOR_j	0.1	0.3	-0.1	0.9	0.5	1.2	-0.5	1.3
LOR_m	2.3	5.3	-1.9	14.2	2.9	7.5	-3.5	9.8
PTHT	1.3	2.9	-0.2	1.7	-1.5	3.8	-3.8	10.7
ERHT	2.5	5.7	-1.6	12.5	1.7	4.4	-0.8	2.3
ERHT:PTHT	2.4	5.4	-2.4	17.9	2.8	7.4	-3.8	10.6
TBN	1.8	4.0	-1.4	10.6	4.8	12.4	-5.5	15.5
PLA	-1.3	3.0	-2.6	19.7	2.0	5.3	-6.1	17.2
LODG	-3.7	8.4	2.4	18.1	-4.2	10.8	-5.3	14.9
CER	2.1	4.7	-[1]	-	0.5	1.3	-	-
SLW	0.1	0.3	-	-	1.2	3.2	-	-
LT	0.8	1.8	-	-	0.8	2.2	-	-

[1]Trait not measured.

(except ERHT and CER) resulted in greater predicted gain for YIELD at the high density than for YIELD at the low density. On the other hand, PTHT, TBN, days to flowering, GRNPLA and, to a small extent, LOV_j and LOR_j were the only traits that reduced BARREN more at the high than the low density.

Evidently, some improvement in YIELD and BARREN at both plant densities would result from indirect selection of traits at the low density. Selection for traits at the low density, however, would not reduce BARREN at the high density as effectively as selection for the same traits at the high density.

Index selection

Traits that exhibited high correlations with yield and barrenness at 96,875 pl/ha and traits found to contribute significantly to prediction equations (Tables 34, 35, 36 and 40 through 52) were used to construct several selection indices with 10% selection intensity. Combinations of traits in individual indices were considered for one or more of the following reasons: 1) they appeared to be the most important in yield determination, 2) they were relatively easy to measure, or 3) they could be measured before harvest and/or without a high-density yield test.

The major difficulty encountered in the construction of selection indices as proposed by Smith (1936) is the assigning of relative economic weights to traits in each index. To facilitate making comparisons of genetic improvement for YIELD from direct selection with that from selection based on the various indices, the economic weight for YIELD was set at unity. The economic weights for the other traits were then assigned relative to YIELD.

Suwantaradon (1974) compared results obtained with five sets of relative economic weights he used to construct 13 selection indices from various combinations of seven traits. For 10 of the 13 indices he constructed, the greatest aggregate genetic advance was observed when all traits were considered equally important and assigned relative economic weights equal to one-half that of yield. Additionally, Suwantaradon (1974) found that indices in which more relative emphasis was placed on yield than on other traits, did not show selection advantages over indices using other sets of relative economic weights. In fact, those indices resulted in less aggregate progress, and those in which all traits received an economic weight of 0.0 and yield was given a weight of 1.0, showed the lowest efficiency of all. In developing selection indices to improve yield potential of BSUL1, therefore, all traits except YIELD were considered equally important and were assigned values equal to one-half that of YIELD; i.e., YIELD was assigned an economic weight of 1.0, and the other traits in the index were given values of 0.5 or -0.5 depending on whether the population mean for the trait was to be increased or decreased be selection. The value 0.5 which was assigned to PROLIF and GRNPLA, for example, means that increasing either of these traits by one unit would be equivalent to increasing YIELD by half of its unit (i.e., 0.5 q/ha). Similarly, the value -0.5 assigned to PSS, SI, SD and all flowering traits, denotes that decreasing any of these traits by one day would be equivalent to direct increase in YIELD of one-half unit.

Selection indices composed of harvest traits (i.e., YIELD, BARREN, GRNPLA, PROLIF) resulted in the greatest aggregate genetic gains of all the indices I developed (Tables 62-69). The greatest genetic contribution, 26.72 q/ha in yield equivalent, resulted from the index including YIELD, BARREN and GRNPLA (Table 63). Additionally, the direct genetic response for all three traits in this index (Table 63) was greater than the response from single-trait selection for these traits (Table 59). This phenomenon was not observed with other indices.

Indices composed of traits strongly associated with yield and barrenness (Tables 65 and 66) resulted in aggregate genetic gains that were about 50% of those obtained with indices that included YIELD and BARREN (Tables 62-64). Indices in which harvest traits were completely excluded (Tables 67-69) exhibited the lowest aggregate genetic advances.

Use of selection indices (Tables 62-69) resulted in correlated responses for traits not included in an index. Without exception, flowering, and flowering-duration traits, TBN, PLA and BARREN were reduced, whereas, YIELD, YIELDP, PROLIF and GRNPLA usually were increased. Lodging percentages (LODG), however, increased. This result likely was a consequence of the relative economic weights used and the high genotypic correlations between LODG and YIELD. When LODG was incorporated into an index (Table 68) it was decreased by 16.29%, but the correlated responses for YIELD and most other traits were small.

My results did not indicate that the superiority of yield equivalent of a selection index increased as the number of traits in the index was

Table 62. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
23.81	YIELD	13.74	YIELDP	14.73
		(0.54)	PROLIF	16.23
			GRNPLA	0.51
	BARREN	-20.15	PTHT	-3.05
		(-0.52)	ERHT	0.76
			ERHT:PTHT	0.01
			TBN	-1.81
			PLA	-87.79
			LODG	7.67
			LOV_j	0.40
			LOV_a	-1.14
			LOV_b	-0.33
			25%ANTH	-1.38
			50%ANTH	-1.33
			75%ANTH	-1.53
			25%SILK	-2.77
			50%SILK	-4.47
			75%SILK	-5.92
			PSS	-3.13
			SI	-3.25
			SD	-2.84

Table 63. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
26.72	YIELD	15.36	YIELDP	17.41
		(0.69)	PROLIF	15.78
			PTHT	-2.85
	BARREN	-22.15	ERHT	0.99
		(-0.49)	ERHT:PTHT	0.01
			TBN	-1.77
	GRNPLA	0.56	PLA	-88.90
		(-3.00)	LODG	8.22
			LOV_j	0.43
			LOV_a	-1.18
			LOV_b	-0.30
			25%ANTH	-1.34
			50%ANTH	-1.28
			75%ANTH	-1.52
			25%SILK	-2.77
			50%SILK	-4.81
			75%SILK	-5.89
			PSS	-3.16
			SI	-3.20
			SD	-2.73

Table 64. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
25.69	YIELD	13.76	YIELDP	11.07
		(0.35)	PROLIF	16.71
			PTHT	-3.33
	BARREN	-20.18	ERHT	0.48
		(-0.71)	ERHT:PTHT	-0.01
			TBN	-1.84
	GRNPLA	0.45	PLA	-84.69
		(4.30)	LODG	6.92
			LOV_j	0.20
	SI	-3.22	LOV_a	-1.13
		(0.61)	LOV_b	-0.49
			25%ANTH	-1.44
			50%ANTH	-1.40
			75%ANTH	-1.56
			25%SILK	-2.75
			50%SILK	-4.45
			75%SILK	-5.91
			PSS	-3.05
			SD	-2.66

Table 65. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
13.56	PROLIF	20.76	YIELD	11.48
		(0.35)	BARREN	-19.10
			YIELDP	12.81
	75%SILK	-6.35	GRNPLA	0.49
		(-0.59)	PTHT	-4.19
			ERHT	0.10
			ERHT:PTHT	0.01
			TBN	-1.55
			PLA	-110.24
			LODG	7.91
			LOV_j	0.58
			LOV_a	-1.66
			LOV_b	-1.04
			25%ANTH	-1.76
			50%ANTH	-1.76
			75%ANTH	-1.98
			25%SILK	-3.17
			50%SILK	-5.24
			PSS	-3.15
			SI	-3.24
			SD	-2.71

Table 66. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
12.38	PROLIF	17.94	YIELD	12.30
		(0.13)	BARREN	-19.47
			YIELDP	13.91
	PSS	-3.41	GRNPLA	0.45
		(-1.51)	PTHT	-3.22
			ERHT	0.34
	SI	-3.40	ERHT:PTHT	0.01
		(-1.46)	TBN	-2.26
			PLA	-82.48
			LODG	8.46
			LOV_j	1.03
			LOV_a	-1.35
			LOV_b	-0.24
			25%ANTH	-1.31
			50%ANTH	-1.37
			75%ANTH	-1.55
			25%SILK	-3.07
			50%SILK	-4.92
			75%SILK	-6.41
			SD	-3.07

Table 67. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
5.86	75%SILK	-5.19	YIELD	5.95
		(-0.43)	BARREN	-11.64
			YIELDP	6.68
	50%ANTH	-2.59	PROLIF	9.36
		(-0.73)	GRNPLA	0.26
			ERHT	-8.54
	PTHT	-3.93	ERHT:PTHT	-0.58
		(-0.41)	TBN	-1.59
			PLA	-48.81
			LODG	-4.42
			LOV_j	0.15
			LOV_a	-0.47
			LOV_b	-0.34
			25%ANTH	-2.55
			75%ANTH	-2.63
			25%SILK	-3.39
			50%SILK	-4.45
			PSS	-1.87
			SI	-1.56
			SD	-1.46

Table 68. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
9.86	75%SILK	-1.44	YIELD	-0.58
		(-0.39)	BARREN	-1.20
			YIELDP	-1.02
	TBN	-1.99	GRNPLA	0.19
		(-0.32)	PTHT	-8.64
			ERHT	-6.72
	LODG	-16.29	ERHT:PTHT	0.00
		(-0.36)	PLA	-129.91
			LOV_j	-0.34
			LOV_a	-0.72
			LOV_b	-2.74
			25%ANTH	-1.21
			50%ANTH	-1.34
			75%ANTH	-1.53
			25%SILK	-1.16
			50%SILK	-1.42
			PSS	-0.06
			SI	-0.31
			SD	0.25

Table 69. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the 23 traits measured at 96,875 pl/ha, and b-values (in parentheses) for traits used in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
4.51	50%SILK	-5.94	YIELD	11.54
		(-0.55)	BARREN	-18.25
			YIELDP	12.77
	SI	-3.08	PROLIF	17.11
		(-0.16)	GRNPLA	0.41
			PTHT	-6.32
			ERHT	-2.32
			ERHT:PTHT	-0.01
			TBN	-2.82
			PLA	-78.01
			LODG	5.32
			LOV_j	0.62
			LOV_a	-1.21
			LOV_b	-0.64
			25%ANTH	-2.49
			50%ANTH	-2.47
			75%ANTH	-2.61
			25%SILK	-4.17
			75%SILK	-6.90
			PSS	-3.58
			SD	-2.92

increased. Rather, they indicated that the superiority of some indices was dependent on the magnitudes of the estimated variance components and relationships among traits in individual indices. Suwantaradon (1974) reported similar observations. The advantages of some indices for yield improvement associated with the addition of traits were small and probably would not warrant the time and effort involved in constructing them. Furthermore, the failure of the selection indices to improve the primary traits, YIELD and BARREN, when compared to advances from single-trait selection, may be due to the relatively high heritability estimates for these traits (i.e., 0.71 and 0.76, respectively) obtained by S_1 progeny testing. Predicted gains from selection for increased GRNPLA at 96,875 pl/ha resulted in an increase of 23.3 q/ha for YIELD and a decrease of 28.1% for BARREN (Table 60). Improvements of these magnitudes were not observed with index selection.

The index composed of YIELD, BARREN and GRNPLA (Table 63) resulted in the greatest genetic gains (i.e., 15.36 q/ha, -22.15% and 0.56 g/dm^2 for YIELD, BARREN and GRNPLA, respectively); however, these traits (especially GRNPLA) are expensive and difficult to measure. Even though the index involving PROLIF and 75%SILK (Table 65) displayed an aggregate genetic advance that was only 50% that obtained for the index involving YIELD, BARREN and GRNPLA, it resulted in an 11.48 q/ha increase in YIELD and a 19.10% decrease in BARREN. Additionally, the index that included PROLIF, PSS and SI resulted in a 12.30 q/ha increase in YIELD and a 19.47% decrease in BARREN. Since the indirect responses for YIELD and BARREN observed with these two indices were comparable to the responses obtained with the index involving YIELD, BARREN and GRNPLA and since the employment of these two indices would be less expensive, one could use either to obtain substantial improvement in yield potential. If one is interested in maximum genetic advance regardless of the economics involved, however, indices composed of the harvest traits, YIELD, BARREN and GRNPLA will result in the greatest aggregate gains.

Traits measured at 42,383 pl/ha that exhibited high correlations with yield and barrenness at 96,875 pl/ha and low-density traits that were found to contribute significantly to prediction equations (Tables 35, 36 and 40 through 52) also were used to construct selection indices with 10% selection intensity. Additionally, indirect genetic responses for YIELD and BARREN at 96,875 pl/ha and genetic responses for traits representative of yield, prolificacy, leaf-orientation, plant size and flowering duration at 42,383 pl/ha were calculated (Tables 70-74).

The index composed of YIELD and PROLIF exhibited the greatest aggregate genetic advance (Table 70). This advance, however, was less than 50% of that obtained with the best index using high-density traits (Table 63). Also, YIELD and BARREN (both measured at the high density) displayed greater indirect genetic responses with four of the five indices composed of low-density traits (Tables 70-74) than did either YIELD or BARREN at the low density. Furthermore, in three of the five indices, the indirect response for YIELD and BARREN exceeded the 11.5 q/ha and 15.1%, respectively, observed for single-trait selection (Table 61). This may be explained partly by the fact that heritabilities for YIELD

Table 70. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the traits measured at 42,383 pl/ha, and b-values (in parentheses) for traits in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
12.84	YIELD	7.44	YIELD[a]	11.88
		(0.52)	BARREN[a]	-14.94
			BARREN	-7.31
	PROLIF	10.80	SECOND	1.72
		(0.32)	LOR_m	0.16
			LODG	5.95
			ERHT	3.05
			TBN	-1.00
			PLA	-128.31
			PSS	-1.36

[a]Measured at 96,875 pl/ha.

Table 71. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the traits measured at 42,383 pl/ha, and b-values (in parentheses) for traits in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
4.62	PROLIF	8.43	YIELD[a]	1.26
		(0.56)	YIELD	3.56
			BARREN[a]	-5.77
	GRNPLA	0.81	BARREN	-7.14
		(-10.83)	SECOND	1.51
			LOR_m	0.05
			LODG	16.05
			ERHT	2.48
			TBA	-0.89
			PLA	-131.20
			PSS	-2.14

[a]Measured at 96,875 pl/ha.

Table 72. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the traits measured at 42,383 pl/ha, and b-values (in parentheses) for traits in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
3.51	75%SILK	-5.36	YIELD[a]	11.41
		(-0.73)	YIELD	5.46
			BARREN[a]	-17.29
	SD	-1.62	BARREN	-6.38
		(0.47)	SECOND	0.93
			LODG	0.62
	LOR_m	0.03	ERHT	-3.80
		(0.61)	TBN	-1.85
			PLA	-216.54
			PSS	-1.21

[a]Measured at 96,875 pl/ha.

Table 73. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the traits measured at 42,383 pl/ha, and b-values (in parentheses) for traits in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
2.62	75%SILK	-5.18	YIELD[a]	11.76
		(-0.40)	YIELD	6.18
			BARREN[a]	-17.34
	LOR_m	0.06	BARREN	-7.14
		(0.35)	SECOND	1.25
			LODG	2.02
			ERHT	-2.28
			TBN	-2.21
			PLA	-165.46
			PSS	-1.52

[a]Measured at 96,875 pl/ha.

Table 74. Expected aggregate genetic advance in yield equivalent from index selection, expected genetic response per cycle in the units of the traits measured at 42,383 pl/ha, and b-values (in parentheses) for traits in the index

	Genetic responses			
	Direct		Indirect	
Aggregate genetic advance	Trait	Response	Trait	Response
2.62	75%SILK	-5.18	YIELD[a]	11.85
		(-0.40)	YIELD	4.15
			BARREN[a]	-17.46
	ERHT:PTHT	0.001	BARREN	-4.78
		(1.25)	PROLIF	6.66
			SECOND	0.86
	LOR_m	0.06	LODG	1.48
		(0.35)	ERHT	-1.33
			TBN	-1.46
			PLA	-184.20
			PSS	-1.02

[a]Measured at 96,875 pl/ha.

and BARREN are significantly greater at the high than at the low density (Table 15).

Index selection for YIELD and PROLIF resulted in slightly greater direct genetic responses for these traits than did single-trait selection. For example, direct genetic responses for YIELD and PROLIF from index selection (Table 70) were 7.44 q/ha and 10.80, respectively, compared to genetic responses from single-trait selection for these traits of 7.3 q/ha and 10.7, respectively (Table 59). With the exception of GRNPLA and 75%SILK in the indices composed of PROLIF and GRNPLA (Table 71) and 75%SILK, SD and LOR_m (Table 72), respectively, direct genetic responses for the traits in the selection indices, Tables 71 to 74, were smaller than genetic responses from single-trait selection for these traits (Table 59).

Ear-to-plant-height ratio (ERHT:PTHT) which contributed significantly to the prediction equations for barrenness (Table 51) was of little value when used in a selection index. Inclusion of ERHT:PTHT in the index with 75%SILK and LOR_m (Table 74) resulted in no selection advantage compared to the index composed of 75%SILK and LOR_m only (Table 74).

Except for LODG, indirect genetic responses were favorable and these responses were of similar magnitudes to those observed with index selection for high-density traits (Tables 62-69).

From examinations of selection indices composed of traits at the low density, it is evident that increased grain yield and reduced barrenness at high plant densities can be achieved via index selection for

YIELD and PROLIF (Table 70) and/or 75%SILK and LOR_m (Table 73) at a low density. Furthermore, similar indirect genetic responses for YIELD at the high density were observed from index selection at either density. For example, observed increases in YIELD (at the high density) were 11.88 and 11.76 q/ha from index selection at the low density for YIELD and PROLIF (Table 71) and 75%SILK and LOR_m (Table 73), respectively; whereas, increases in YIELD (at the high density) from index selection for PROLIF and 75%SILK (Table 65) and PROLIF, PSS and SI (Table 66) at the high density were 11.48 and 12.30 q/ha, respectively. Since the indirect genetic responses for YIELD at the high density observed with indices from the low density were comparable to the responses obtained with the indices at the high density, and since the mechanics of low-density selection would be easier and less expensive, one could use low-density indices to improve yield potential in BSUL1.

Traits that contributed significantly to the selection indices (Tables 62-69) also were used to construct modified selection indices as proposed by Pesek and Baker (1969). This modification of index selection would be useful in recurrent selection programs (Pesek and Baker, 1970). Therefore, I examined the effectiveness of such index selection in simultaneous improvement of multiple traits in an S_1 testing program (Tables 75-78). A cycle of selection for this scheme can be completed within two years if two seasons per year are available. Yield and other traits would be measured in the same season.

Goals of improvement at the final stage of selection for YIELD, BARREN, GRNPLA, PROLIF, LODG, SI, TBN and LOR_m were set at 100 q/ha, 0.0%,

Table 75. Expected genetic responses per cycle from the application of a modified selection index in recurrent selection using S_1 testing at 96,875 pl/ha with a 10% selection intensity

	Traits	
	YIELD	BARREN
Population mean	38.3	35.5
Selection goals	100.0	0.0
Desired genetic gains	61.7	-35.5
Phenotypic weights (b-values)	2.40	1.31
Direct genetic responses	10.83	-6.13

Table 76. Expected genetic responses per cycle from the application of a modified selection index in recurrent selection using S_1 testing at 96,875 pl/ha with a 10% selection intensity

	Traits		
	YIELD	BARREN	GRNPLA
Population mean	38.3	35.5	1.0
Selection goals	100.0	0.0	2.0
Desired genetic gains	61.7	-35.5	1.0
Phenotypic weights (b-values)	1.61	1.17	15.69
Direct genetic responses	12.48	-7.06	0.20

Table 77. Expected genetic responses per cycle from the application of a modified selection index in recurrent selection using S_1 testing at 96,875 pl/ha with a 10% selection intensity

	Traits			
	YIELD	BARREN	GRNPLA	SI
Population mean	38.3	35.5	1.0	7.5
Selection goals	100.0	0.0	2.0	1.0
Desired genetic gains	61.7	-35.5	1.0	-6.5
Phenotypic weights (b-values)	1.62	1.56	16.66	-2.29
Direct genetic responses	12.42	-7.20	0.20	-1.32

Table 78. Expected genetic responses per cycle from the application of a modified selection index in recurrent selection using S_1 testing at 96,875 pl/ha with a 10% selection intensity

	Traits		
	YIELD	BARREN	LODG
Population mean	38.3	35.5	20.8
Selection goals	100.0	0.0	2.0
Desired genetic gains	61.7	-35.5	-18.8
Phenotypic weights (b-values)	-0.46	1.21	0.48
Direct genetic gains	-14.27	22.67	-1.63

2.0 g/dm^2, 120.0, 2.0%, 1.0 day, 5.0 and 4.0, respectively. With 10% selection intensity, YIELD and BARREN (Table 75) would approach the goals for improvement in 6 cycles of selection. When GRNPLA and SI were included in the index (Tables 76 and 77) the selection goals would be achieved in 5 cycles. Additionally, when LODG was included in the index in an effort to increase the agronomic acceptability of BSUL1, the progress for YIELD and BARREN was in a negative direction initially and 12 cycles of selection would be required to reach the desired goal. Single-trait selection, however, would require only 4 cycles to attain the goal of improvement for YIELD (Table 59). Therefore, simultaneous improvement of several traits of BSUL1 could take 25 to 300% longer than improvement of YIELD to 100 q/ha through selection for YIELD *per se*.

Two indices composed of one trait from the low and one trait from the high density are presented in Tables 79 and 80. For both indices, an indirect genetic response for YIELD at the high density was attained by simultaneous selection of these traits at both densities. This advance in YIELD for the index involving PROLIF and SI was comparable to the advance in YIELD from the best index at the high density (Table 63). A second index composed of two traits (i.e., LOR_m and TBN) which are measured very easily, resulted in an indirect genetic response for YIELD at the high density of 5.85 q/ha. These data indicate that the yield potential of BSUL1 could be increased simply and inexpensively by selection for easily measured traits. The increased number of cycles required for the desired improvement, however, considerably reduces the merits of such an index.

Table 79. Expected genetic responses per cycle from the application of a modified selection index using traits from two densities with a 10% selection intensity

	PROLIF	SI	YIELD
	42,383 pl/ha	96,875 pl/ha	96,875 pl/ha
Population mean	91.2	7.5	13.96[a]
Selection goals	120.0	1.0	
Desired genetic gains	28.8	-6.5	
Phenotypic weights (b-values)	0.56	0.66	
Direct genetic gains	14.67	-3.31	

[a]Indirect genetic response from selection for index of PROLIF and SI.

Table 80. Expected genetic responses per cycle from the application of a modified selection index using traits from two densities with a 10% selection intensity

	LOR_m	TBN	YIELD
	42,383 pl/ha	96,875 pl/ha	96,875 pl/ha
Population mean	2.1	16.2	5.85[a]
Selection goals	4.0	5.0	
Desired genetic gains	1.9	-11.2	
Phenotypic weights (b-values)	10.31	-0.70	
Direct genetic goals	0.63	-3.77	

[a]Indirect genetic response from the selection index of LOR_m and TBN.

It is evident that maximum progress for improved yield potential and reduced barrenness at high densities will result from selection for increased yield and reduced barrenness _per se_ at high plant densities. I believe, however, there is sufficient data warranting selection at a low density. Results from my study indicated high-density yield improvement via selection at the low density was approximately 75 to 100% as efficient as selection at the high density. This fact, accompanied by the problems encountered with high-density testing (i.e., insufficient S_1 seed supplies, difficulty in trait measurement resulting from the proximity of plants and a general requirement of higher management levels) increase the attractiveness of low-density selection.

I propose improving the density tolerance of BSUL1 via a recurrent selection program for yield and prolificacy at low stand levels (i.e., 45,000 to 50,000 pl/ha). Two-row plots with two replications grown at three locations would require less than 350 kernels and should minimize the bias from genotype x environment. Index selection for yield and prolificacy should result in 11.88 q/ha/cycle increase in high-density yield (Table 70). Employment of this index should also result in reduced barrenness, tassel size, plant-leaf area, and flowering duration and a slight improvement in canopy orientation. Increased ear height and lodging, however, will accompany increases in yield and prolificacy. To insure agronomic acceptability, therefore, it may be necessary to reduce the selection intensity to a level that will allow selection of plants with sufficient stalk quality (i.e., 15 to 20%). Remnant seed from the selected S_1 lines will be recombined the following season. Approximately 200-300 plants are self-pollinated and the cycle is repeated. This program which requires three seasons or two years if a winter nursery is available, should result in effective yield improvement in BSUL1.

Assuming yield tests are not feasible for this population improvement program, an alternative procedure, i.e., recurrent selection for early flowering (75%SILK) and mature visual canopy orientation (LOR_m) may be adopted. S_1 lines would be grown in two-row plots with two replications in the breeding nursery. Index selection for reduced 75%SILK and increased LOR_m should result in 11.76 q/ha/cycle increase in high-density yield (Table 73). Correlated responses for reduced barrenness, tassel branch number, plant leaf area, flowering duration and ear height should accompany this index selection for 75%SILK and LOR_m.

Additionally, the increase in lodging was only 2.02% for this index compared with 5.95% for the index composed of YIELD and PROLIF (Tables 70 and 73). Assuming the genotypes can be rated for LOR_m at anthesis and silking data can be rapidly analyzed, selected lines could be recombined in the same season. This would allow completion of one cycle per year and, therefore, result in greater efficiency of the program. If, however, selection for improved agronomic desirability (i.e., reduced lodging) is necessitated, completion of a cycle will require two years. After a few cycles of selection or when flowering dates and leaf orientation are satisfactory, prolificacy should be added to the model to increase the effectiveness of selection for improved yield potential. Index selection (i.e., 75%SILK and LOR_m) should be effective in one environment because of small genotype x environment variance components for these traits (Tables 16 and 17).

SUMMARY AND CONCLUSIONS

I used two sets of 144 S_1 families from Iowa Upright Leaf Synthetic #1 (BSUL1) to determine the association between density tolerance and various morphological and physiological traits and to determine whether or not these traits could be used in a maize breeding program. My study was conducted for three years at one location. I measured the variability and estimated heritabilities for 30 traits at a low plant density (i.e., 42,383 pl/ha) and 27 traits at a high plant density (i.e., 96,875 pl/ha) in an attempt to characterize BSUL1 under near-optimum and stress conditions.

I estimated phenotypic, genotypic and error correlations for all pairs of traits. Additionally, I fit multiple regression models to examine the effectiveness of groups of traits in explaining the variability for yield and barrenness at both plant densities. Also, the data were subjected to factor analysis in an effort to obtain a better understanding of the common causative influences between various traits. Finally, I examined progress from selection for each trait and I developed several selection indices to determine the most effective procedure for improving the density tolerance of BSUL1.

My data demonstrated there was adequate variability within BSUL1 to permit successful selection for reduced barrenness and increased grain yield. Furthermore, heritability estimates for most traits were high (0.31 ± 0.11 to 0.91 ± 0.02) indicating the major portion of this variability was genotypic. The heritability estimate for grain per unit leaf area at the low density, however, was not significantly different from zero (0.14±0.14). Heritability estimates on an entry-mean basis were generally larger at the high than at the low plant density. For example, heritabilities for yield were 0.71±0.05 at the high density and 0.52±0.08 at the low density.

Correlations indicated that barrenness, prolificacy, grain per unit leaf area and all flowering traits (i.e., days to flowering, pollen-shed-to-silking interval, silking interval and silking delay) were highly correlated with yield (absolute r-values ranged from 0.34 to 0.88 at the high density and from 0.19 to 0.73 at the low density). Correlations between yield and tassel branch number, plant-leaf area and lodging at the high density, and plant and ear heights, tassel branch number, mature canopy-orientation rating and lodging at the low density were significant statistically but of small magnitudes (absolute r-values ranged from 0.16 to 0.24). With the exception of mature visual rating, canopy-orientation traits were not related to density tolerance of BSUL1.

Multiple-regression techniques and factor analysis also demonstrated that harvest (i.e., yield per plant, prolificacy, percent second-ear grain and grain per unit leaf area) and flowering traits (i.e., days to flowering and flowering duration) were the most important in determining yield and barrenness at high plant densities. Canopy-orientation traits and plant-stature traits (i.e., heights, plant leaf area, etc.) were not important in explaining the variability for yield and barrenness.

Stepwise multiple regression analysis indicated that barrenness, prolificacy, grain per leaf area, days to flowering and lodging percentage were the most important traits for predicting grain yield at the high plant density.

I used carbon dioxide exchange rate (CER) of leaf sections from excised leaves to estimate the net photosynthetic efficiency of 64 random S_1 lines from BSUL1. From these data, I concluded that the variability for CER was sufficient to permit successful selection for the trait. CER, however, explained less than 5% of the variation for grain yield and, therefore, was not limiting yielding ability of BSUL1.

Most traits exhibited high predicted gains from single-trait selection (i.e., 4.4 to 122.4% of the population mean). Additionally, I found that the yield potential of BSUL1 could be improved by indirect selection for traits highly correlated with yield or barrenness (i.e., prolificacy, grain per unit leaf area, days to silk emergence, pollen-shed-to-silking interval, silking interval and silking delay). Selection indices composed of harvest traits resulted in the greatest aggregate genetic gains and improvement in yield *per se* (i.e., 12.4 to 26.7 q/ha). Comparable progress, however, can be realized by selecting for increased prolificacy and early flowering dates (i.e., days to 75% silk emergence).

Finally, I concluded that progress for improved yield potential and reduced barrenness can be realized from selection at low plant densities. Predicted gains in yield at the high density resulting from selection for grain per unit leaf area, days to 75% silk emergence, silking interval, silking delay and prolificacy were 17.7, 11.4, 11.1, 10.6 and 10.5 q/ha, respectively. Additionally, two selection indices composed of traits measured at the low density (i.e., yield and prolificacy; and days to 75% silk emergence and mature visual canopy-orientation rating) resulted in increases of yield at the high density of 11.9 and 11.8 q/ha, respectively.

Two recurrent selection procedures involving S_1 testing were proposed for improving the density tolerance of BSUL1 via index selection at low densities:

1) selection for yield and prolificacy in three environments, and
2) selection for days to 75% silk emergence and mature visual canopy orientation.

LITERATURE CITED

Allard, R. W. 1960. Principles of plant breeding. John Wiley and Sons, Inc., New York.

Anderson, I. C. 1971. Possible practical applications of chemical pollen control in corn and sorghum seed production. Corn and Sorghum Res. Conf. Proc. 26:22-26.

Anderson, M. C., and O. T. Denmead. 1969. Short wave radiation on inclined surfaces in model plant communities. Agron. J. 61:867-872.

Andrew, R. H. 1967. Influence of season, population, and spacing on axillary bud development of sweet corn. Agron. J. 59:355-358.

Ariyanayagam, R. P., C. L. Moore, and V. R. Carangal. 1974. Selection for leaf angle in maize and its effect on grain yield and other characters. Crop Sci. 14:551-556.

Barnes, D. L., and D. G. Woolley. 1969. Effect of moisture stress at different stages of growth. I. Comparison of a single-eared and a two-eared corn hybrid. Agron. J. 61:788-790.

Bauman, L. F. 1960. Relative yields of first (apical) and second ears of semi-prolific southern corn hybrids. Agron. J. 52:220-222.

Buren, L. L. 1970. Plant characteristics associated with barrenness in maize. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Buren, L. L., J. J. Mock, and I. C. Anderson. 1974. Morphological and physiological traits in maize associated with tolerance to high plant density. Crop Sci. 14:426-429.

Campbell, C. M. 1964. Influence of seed formation of corn on accumulation of vegetative dry matter and stalk strength. Crop Sci. 4:31-34.

Cardwell, V. B. 1967. Physiological and morphological response of corn genotypes to planting date and plant population. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Cattell, R. B. 1965. Factor analysis:an introduction to essentials. I. The purpose of underlying models. Biometrics 21:190-215.

Chinwuba, P. M., C. O. Grogan, and M. S. Zuber. 1961. Interaction of detasseling, sterility and spacing on yield of maize hybrids. Crop Sci. 1:279-280.

Cochran, W. G., and G. M. Cox. 1957. Experimental designs. 2nd ed. John Wiley and Sons, Inc., New York.

Collins, W. K., and W. A. Russell. 1965. Development of the second ear of thirty-six hybrids of corn belt _Zea mays_ L. Iowa State J. Sci. 40:35-50.

Collins, W. K., W. A. Russell, and S. A. Eberhart. 1965. Performance of two-ear type of corn belt maize. Crop Sci. 5:113-116.

Comstock, R. E., and R. H. Moll. 1963. Genotype-environment interactions. p. 164-194. _In_ H. F. Robinson (ed.) Statistical genetics and plant breeding. NAS-NRC, Publication 982.

Crosbie, T. M. 1976. Variability of net photosynthesis in Iowa Stiff Stalk Synthetic and relationship of net photosynthesis with various traits. Unpublished M.S. thesis. Library, Iowa State University, Ames, Iowa.

Crosbie, T. M., J. J. Mock, and R. B. Pearce. 1977. Variability and selection advance for photosynthesis in Iowa Stiff Stalk Synthetic maize population. Crop Sci. 17:511-514.

Denmead, O. T., and R. H. Shaw. 1960. The effect of soil moisture stress at different stages of growth on the development and yield of corn. Agron. J. 52:272-274.

Draper, N. R., and H. Smith. 1967. Applied regression analysis. John Wiley and Sons, Inc., New York.

Duncan, W. G. 1958. The relation between corn populations and yield. Agron. J. 50:82-84.

Duncan, W. G. 1969. Cultural manipulation for higher yields. p. 327-339. _In_ R. C. Dinauer (ed.) Physiological aspects of crop yield. Amer. Soc. Agron., Madison, Wisconsin.

Duncan, W. G. 1971. Leaf angle, leaf area, and canopy photosynthesis. Crop Sci. 11:482-485.

Duncan, W. G., W. A. Williams, and R. S. Loomis. 1967. Tassels and the productivity of maize. Crop Sci. 7:37-39.

Dungan, G. H., A. L. Lang, and J. W. Pendleton. 1958. Corn plant population in relation to soil productivity. Adv. Agron. 10:435-474.

Duvick, D. N. 1958. Yield and other agronomic characteristics of cytoplasmically pollen sterile corn hybrids compared to their normal counterparts. Agron. J. 50:121-125.

Duvick, D. N. 1974. Continuous backcrossing to transfer prolificacy to a single-eared inbred line of maize. Crop Sci. 14:69-71.

Duvick, D. N., and S. W. Noble. 1969. Testing the hybrid x row width interaction. Agron. Abstr. 1969:5.

Earley, E. B. 1965. Relative maximum yield of corn. Agron. J. 57:514-515.

Earley, E. B., R. J. Miller, G. L. Reichert, R. H. Hageman, and R. D. Seif. 1966. Effects of shade on maize production under field conditions. Crop Sci. 6:1-7.

Earley, E. B., W. A. McIlrath, R. D. Seif, and R. H. Hageman. 1967. Effects of shade applied to different stages of plant development on corn production. Crop Sci. 7:151-156.

Eckert, R. T., and R. D. Westfall. 1975. The factor analysis of multivariate data systems. Northwestern Forest Tree Improvement Conf. Proc. 22:41-52.

El-Lakany, M. A., and W. A. Russell. 1971. Relationships of maize characters with yield in testcrosses of inbreds at different plant densities. Crop Sci. 11:698-701.

Fakorede, M. A. B. 1975. Productivity of maize (Zea mays L.) as affected by plant density and simulated vertical leaf orientation. Unpublished M.S. thesis. Library, Iowa State University, Ames, Iowa.

Fakorede, M. A. B. 1977. Direct and correlated responses to recurrent selection for grain yield in maize breeding populations. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Fakorede, M. A. B., C. S. Smith, and J. J. Mock. 1978. Application of factor analysis to maize breeding. Maydica 23:in press.

Freeman, W. H. 1955. Evaluating hybrids in the south. Hybrid Corn Industry-Research Ann. Conf. Proc. 10:24-31.

Grogan, C. O. 1956. Detasseling responses in corn. Agron. J. 48:247-249.

Hanson, W. D., and H. W. Johnson. 1957. Methods for calculating and evaluating a general selection index obtained by pooling information from two or more experiments. Genetics 42:421-432.

Hicks, D. R., and R. E. Stucker. 1972. Plant density effect on grain yield of corn hybrids diverse in leaf orientation. Agron. J. 64:484-487.

Hinkle, D. A., and J. D. Garrett. 1961. Corn fertilizer and spacing experiments. Arkansas Agricultural Exp. Sta. Bul. 635.

Hopper, N. W. 1970. The evaluation of upright leaves and the use of sucrose and glutomate in increasing the yield of corn. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Hunter, R. B., T. B. Daynard, D. J. Hume, J. W. Tanner, J. D. Curtis, and L. W. Kannenberg. 1969. Effect of tassel removal on grain yield in corn. Crop Sci. 9:405-406.

Johnson, H. W., H. F. Robinson, and R. E. Comstock. 1955. Genotypic and phenotypic correlations in soybeans and their implications in selection. Agron. J. 47:477-483.

Josephson, L. M. 1957. Breeding for early prolific hybrids. Hybrid Corn Industry-Research Ann. Conf. Proc. 12:71-79.

Josephson, L. M., H. C. Kincer, and B. G. Harville. 1976. Selection studies for low ear placement in corn. Corn and Sorghum Res. Conf. Proc. 31:85-97.

Jugenheimer, R. W. 1976. Corn improvement, seed production, and uses. John Wiley and Sons, Inc., New York.

Kaiser, H. F. 1958. The varimax criterion for analytical rotation of factor analysis. Psychometrika 23:187-200.

Kiesselbach, T. A. 1950. Progressive development and seasonal variations in the corn crop. Nebraska Agricultural Exp. Sta. Res. Bul. 166.

Kohnke, H., and S. R. Miles. 1951. Rates and patterns of seedling corn on high fertility land. Agron. J. 43:483-493.

Lang, A. L., J. W. Pendleton, and G. H. Dungan. 1956. Influence of population and nitrogen levels on yield and oil content of nine corn hybrids. Agron. J. 48:284-289.

Lee, J., and P. J. Kaltsikes. 1973. Multivariate statistical analysis of grain yield and agronomic characters in Durum wheat. Theor. and Appl. Genetics 43:226-231.

Leonard, W. H., and T. A. Kiesselbach. 1932. The effect of the removal of tassels on the yield of corn. Amer. Soc. Agron. J. 24:415-416.

Lonnquist, J. H., and R. W. Jugenheimer. 1943. The success of pollination in corn. Amer. Soc. Agron. J. 35:923-933.

Loomis, R. S., W. A. Williams, W. G. Duncan, A. Dovrat, and F. Nunez. 1968. Canopy architecture at various population densities and the growth and grain yield of corn. Crop Sci. 8:303-308.

Meyer, D. W. 1970. Use of male sterility for increasing the population tolerance of corn (Zea mays L.). Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Mock, J. J., and L. L. Buren. 1972. Classification of maize (Zea mays L.) inbreds for population tolerance by general combining ability. Iowa State J. Sci. 46:395-404.

Mock, J. J., and S. H. Schuetz. 1974. Inheritance of tassel branch number in maize. Crop Sci. 14:885-888.

Mock, J. J., and R. B. Pearce. 1975. An ideotype of maize. Euphytica 24:613-623.

Mode, C. J., and H. F. Robinson. 1959. Pleitropism and the genetic variances and covariances. Biometrics 15:518-527.

Moll, R. H., and E. J. Kamprath. 1977. Effects of population density upon agronomic traits associated with genetic increases in yield Zea mays L. Agron. J. 69:81-84.

Monteith, J. L. 1965. Light distribution and photosynthesis in field crops. Ann. Bot. N.S. 29:17-37.

Monteith, J. L. 1969. Light interception and radioactive exchange in crop stands. p. 89-140. In R. C. Dinauer (ed.) Physiological aspects of crop yield. Amer. Soc. Agron., Madison, Wisconsin.

Montgomery, F. G. 1911. Correlation studies in corn. Nebraska Exp. Sta. Ann. Report 24:108-159.

Morrison, D. F. 1967. Multivariate statistical methods. McGraw-Hill Co., Inc., New York.

Moss, D. N., and H. T. Stinson. 1961. Differential response of corn hybrids to shade. Crop Sci. 1:416-418.

Mulamba, N. N. 1977. Improvement of yield potential in Eto Blanco maize (Zea mays L.) population through breeding for morphological and physiological traits. Unpublished M.S. thesis. Library, Iowa State University, Ames, Iowa.

Ottaviano, E., A. Camussi, V. Deleo, and M. S. Gorla. 1975. Factor analysis of ear and plant development in maize. Maydica 20:21-37.

Pearce, R. B., J. J. Mock, and T. B. Bailey. 1975. Rapid method for estimating leaf area per plant in maize. Crop Sci. 15:691-694.

Pearce, R. B., T. M. Crosbie, and J. J. Mock. 1976. A rapid method for measuring net photosynthesis of excised leaves by using air-sealed chambers. Iowa State J. of Res. 51:25-33.

Pendleton, J. W., and R. D. Seif. 1961. Plant population and row spacing studies with brachytic-2 dwarf corn. Crop Sci. 1:433-435.

Pendleton, J. W., G. E. Smith, S. R. Winter, and I. J. Johnson. 1968. Field investigations of the relationships of leaf angle in corn (Zea mays L.) to grain yield and apparent photosynthesis. Agron. J. 60:422-424.

Pepper, G. E. 1974. The effect of leaf orientation and plant density on the yield of maize (Zea mays L.). Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Pesek, J., and R. J. Baker. 1969. Desired improvement in relation to selection indices. Can. J. Plant Sci. 49:803-804.

Pesek, J., and R. J. Baker. 1970. An application of index selection to the improvement of self-pollinated species. Can. J. Plant Sci. 50:267-276.

Pesek, J., and R. J. Baker. 1971. Comparison of predicted and observed responses to selection for yield in wheat. Can. J. Plant Sci. 5:187-192.

Prine, G. M. 1961. A factor to be considered in growing corn. Soils and Crop Sci. Soc. of Florida Proc. 21:221-228.

Prine, G. M., and V. N. Schroder. 1964. Above soil environment limits yields of semiprolific corn as plant population increases. Crop Sci. 4:361-362.

Robins, J. S., and C. E. Domingo. 1953. Some effects of severe soil moisture deficits at specific growth stages of corn. Agron. J. 45:618-621.

Russell, W. A. 1968. Testcrosses of one- and two-ear types of corn belt maize inbreds. I. Performance at four plant stand densities. Crop Sci. 8:244-247.

Russell, W. A. 1972. Effect of leaf angle on hybrid performance in maize (Zea mays L.). Crop Sci. 12:90-92.

Russell, W. A. 1974. Comparative performance for maize hybrids representing different eras of maize breeding. Corn and Sorghum Res. Conf. Proc. 29:81-101.

Russell, W. A., and S. A. Eberhart. 1968. Testcrosses of one- and two-ear types of corn belt maize inbreds. II. Stability of performance in different environments. Crop Sci. 8:248-251.

Russell, W. A., and C. L. Prior. 1975. Stability of yield performance of nonprolific and prolific maize hybrids. Iowa State J. Res. 50:17-27.

Rutger, J. N., and L. V. Crowder. 1967. Effect of high plant density on silage and grain yield of six corn hybrids. Crop Sci. 7: 182-184.

Saeki, T. 1960. Interrelationships between leaf amount, light distribution and total photosynthesis in a plant community. Bot. Mag. Tokyo 73:55-63.

Sanford, J. O., C. O. Grogan, H. V. Jordan, and P. A. Sarvella. 1965. Influence of male-sterility on nitrogen utilization in corn, Zea mays L. Agron. J. 57:510-583.

Sass, J. E., and F. A. Loeffel. 1959. Development of axillary buds in maize in relation to barrenness. Agron. J. 51:484-486.

Sayre, J. D., V. H. Morris, and F. D. Richey. 1931. The effect of preventing fruiting and of reducing the leaf area on the accumulation of sugars in the corn stem. J. Amer. Soc. Agron. 23:751-753.

Schwanke, R. K. 1965. Alteration of reproductive attributes of corn varieties by population and detasseling. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Shaw, R. H., and W. E. Loomis. 1950. Bases for the prediction of corn yields. Plant Physiology 25:225-244.

Shaw, R. S., and H. C. S. Thom. 1951. On the phenology of field corn, silking to maturity. Agron. J. 43:541-546.

Simmonds, N. W. 1973. Plant breeding. Phil. Trans. R. Soc. Ser. B., Lond. 267:145-146.

Smith, H. F. 1936. A discriminant function for plant selection. Ann. Eug. 7:240-250.

Sowell, W. F., A. J. Ohlrogge, and O. E. Nelson, Jr. 1961. Growth and fruiting of compact and Hy Normal corn types under a high population stress. Agron. J. 53:25-28.

Steel, R. G. D., and J. H. Torrie. 1960. Principles and procedures of statistics. McGraw-Hill Book Co., Inc., New York.

Stickler, F. C. 1964. Row width and plant population studies with corn. Agron. J. 56:438-441.

Stinson, H. T., and D. N. Moss. 1960. Some effects of shade upon corn hybrids tolerant and intolerant to dense planting. Agron. J. 52:482-484.

Subandi, and W. A. Compton. 1974. Genetic studies in an exotic population of corn (Zea mays L.) grown under two plant densities. II. Choice of a density environment for selection. Theor. Appl. Genet. 44:193-198.

Suwantaradon, K. 1974. Simultaneous selection for several agronomic characters in the BSSS2 maize population by means of selection indices. Unpublished Ph.D. dissertation. Library, Iowa State University, Ames, Iowa.

Suwantaradon, K., S. A. Eberhart, J. J. Mock, J. C. Owens, and W. D. Guthrie. 1975. Index selection for several agronomic traits in the BSSS2 maize population. Crop Sci. 15:827-833.

Tatum, L. A. 1954. Breeding for drought and heat tolerance. Hybrid Corn Industry-Research Ann. Conf. Proc. 9:22-34.

Tormunde, D. E., D. B. Shank, and V. A. Dirks. 1963. Effects of population levels on yield and maturity of maize hybrids grown on the northern great plains. Agron. J. 55:551-555.

Timmons, D. R., R. F. Holt, and J. T. Moraghan. 1966. Effect of corn populations on yield, evapotranspiration, and water-use efficiency in the northwest Corn Belt. Agron. J. 58:429-432.

Troyer, A. F., and W. L. Brown. 1976. Selection for early flowering in corn:Seven late synthetics. Crop Sci. 16:767-772.

Van Reen, R., and W. R. Singleton. 1952. Sucrose content in the stalks of maize inbreds. Agron. J. 44:610-614.

Wallace, D. H., J. L. Ozbun, and H. M. Munger. 1972. Physiological genetics of crop yield. Adv. Agron. 24:97-146.

Whigham, D. K., and D. G. Woolley. 1974. Effect of leaf orientation, leaf area, and plant density on corn production. Agron. J. 66:482-486.

Winter, S. R., and A. J. Ohlrogge. 1973. Leaf angle, leaf area, and corn (Zea mays L.) yields. Agron. J. 65:395-397.

Woolley, D. G., N. P. Barasco, and W. A. Russell. 1962. Performance of four corn hybrids in single cross hybrids as influenced by plant density and spacing pattern. Crop Sci. 2:441-444.

Zuber, M. S., and W. L. Decker. 1956. Effects of 1954 drought on corn. Missouri Agricultural Exp. Sta. Res. Bul. 604.

Zuber, M. S., and C. O. Grogan. 1956. Rates of planting studies with corn. Missouri Agricultural Exp. Sta. Res. Bul. 610.

Zuber, M. S., C. O. Grogran, and O. V. Singleton. 1960. Rate of planting studies with prolific and single-ear hybrids. Missouri Agricultural Exp. Sta. Res. Bul. 737.

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APPENDIX

Appendix Table 1. PROLIF (prolificacy), BARREN (percent barren plants), YIELD (grain yield), YIELDP (grain per plant) and GRNPLA (grain per unit leaf area) for 144 random S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
1	236	53.5	48.2	37.9	42.8	1.2
2	237	73.0	27.0	46.2	49.3	1.1
3	239	72.0	28.4	39.0	44.2	0.9
4	242	28.0	72.3	26.1	29.7	1.1
5	244	74.4	25.9	38.6	42.6	1.0
6	245	81.2	19.1	54.5	57.3	1.4
7	246	45.4	57.4	27.3	32.2	0.7
8	247	83.1	17.2	49.3	53.0	1.3
9	248	72.8	27.8	41.4	45.3	0.9
10	249	77.2	26.8	45.6	47.9	1.1
11	250	59.2	42.1	35.5	38.1	1.0
12	253	57.7	42.7	35.4	37.9	0.7
13	254	58.8	40.7	31.7	37.3	1.1
14	255	83.3	16.1	57.0	64.3	1.4
15	257	80.3	19.4	49.1	55.7	1.4
16	258	89.1	10.6	44.1	48.9	1.2
17	259	74.8	24.9	39.1	43.9	0.9
18	260	39.8	59.9	24.6	25.8	0.7
19	261	62.2	37.4	38.3	41.0	0.8
20	262	86.9	12.8	55.7	62.8	1.3
21	265	73.9	26.1	39.9	43.1	0.9
22	266	56.6	43.1	29.4	34.7	0.9

[a]Measured in 1974 and 1975.

Appendix Table 1 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
23	268	53.8	45.9	38.9	41.2	0.9
24	270	65.5	34.2	44.6	51.4	1.1
25	272	80.2	19.8	45.5	55.1	1.8
26	274	73.7	26.1	38.1	52.6	1.6
27	275	76.2	24.0	50.2	53.1	1.3
28	276	68.0	32.2	37.5	40.2	0.9
29	278	69.1	31.0	43.1	45.4	1.0
30	281	68.9	31.2	43.0	55.1	1.3
31	282	73.6	26.5	60.2	63.8	1.3
32	283	66.0	34.1	39.4	43.6	1.1
33	284	46.7	53.7	29.1	33.7	0.6
34	285	67.2	32.9	38.4	46.0	1.1
35	286	60.4	39.7	33.3	36.7	0.8
36	287	75.1	25.1	47.1	48.5	1.2
37	288	65.0	35.1	43.0	45.8	1.3
38	289	76.3	28.7	36.8	43.4	1.0
39	291	62.5	37.8	36.7	40.1	1.0
40	292	55.6	44.7	30.2	36.0	0.6
41	294	46.7	53.5	22.2	24.7	0.5
42	295	63.3	37.0	32.9	34.1	0.9
43	298	48.2	52.0	24.7	27.0	0.8
44	299	43.9	56.4	23.5	25.4	0.5
45	300	80.6	20.0	40.7	45.9	0.9
46	301	80.3	20.0	42.1	50.7	1.3
47	302	40.3	61.0	23.3	24.7	0.8
48	305	51.7	48.6	29.4	33.7	0.9
49	306	76.3	23.4	39.4	43.3	1.1
50	307	85.3	15.5	51.3	59.6	1.2
51	310	46.8	53.0	25.7	28.7	1.0

Appendix Table 1 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
52	311	87.1	13.7	56.0	59.2	1.2
53	314	67.3	32.6	38.1	42.1	1.1
54	315	85.1	14.8	48.0	54.8	0.9
55	316	79.7	21.1	43.6	51.7	1.1
56	318	75.4	24.4	44.0	50.5	0.9
57	319	45.1	55.0	25.7	28.1	0.6
58	320	77.3	24.5	49.4	54.4	1.1
59	325	74.3	24.3	28.8	34.1	1.0
60	326	54.8	45.1	29.8	31.4	1.0
61	327	65.7	34.1	37.8	42.5	0.9
62	328	64.4	35.2	46.6	50.5	1.0
63	329	70.2	29.8	32.8	37.4	0.9
64	330	71.0	29.0	34.5	32.4	0.9
65	331	84.8	15.1	59.2	60.8	1.2
66	336	86.1	13.8	56.5	64.2	1.3
67	337	90.3	9.6	60.4	66.1	1.4
68	343	86.5	13.4	47.9	52.7	1.0
69	345	74.2	27.0	45.0	51.8	0.9
70	346	67.9	32.0	36.9	39.4	1.2
71	347	69.4	30.5	41.7	44.8	1.2
72	349	57.3	42.6	30.0	34.3	1.1
73	350	64.6	35.3	33.8	34.1	0.9
74	351	76.8	22.9	51.0	55.4	1.3
75	354	65.5	35.5	35.5	38.3	0.9
76	355	50.6	49.4	26.9	30.5	0.5
77	356	33.2	66.8	20.6	21.4	0.8
78	358	94.3	6.8	57.2	58.1	1.1
79	360	43.5	56.5	20.6	24.3	1.0
80	361	62.4	36.9	39.9	46.9	1.4

Appendix Table 1 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
81	364	51.3	49.0	30.7	34.2	0.8
82	365	76.3	24.7	38.2	45.5	0.9
83	369	81.5	18.5	46.3	50.2	1.2
84	370	65.7	34.4	43.7	46.2	1.1
85	372	63.0	36.9	34.7	38.4	0.7
86	373	71.5	28.3	42.9	49.7	1.0
87	374	36.7	63.3	21.0	24.6	0.6
88	377	39.8	60.3	23.9	26.3	0.8
89	378	62.2	37.9	37.7	41.5	0.9
90	380	64.7	35.4	33.5	38.4	1.1
91	381	43.9	56.1	24.4	27.1	0.6
92	382	66.6	33.5	40.6	47.4	1.1
93	383	50.5	49.8	37.2	39.2	0.8
94	384	79.0	21.1	49.8	52.6	1.1
95	385	70.0	30.1	42.2	47.3	1.4
96	388	57.9	42.2	32.3	35.3	1.1
97	389	80.6	21.3	55.7	63.1	1.4
98	390	58.0	41.6	32.5	36.4	1.0
99	392	64.8	35.2	38.3	45.6	1.1
100	396	73.8	28.2	41.5	46.5	0.9
101	397	55.2	44.7	41.3	44.5	1.3
102	400	39.3	60.7	29.0	30.1	0.8
103	401	67.5	32.5	40.4	44.8	1.1
104	402	67.1	30.3	47.4	56.2	1.3
105	404	54.1	46.2	37.7	39.2	0.9
106	408	79.3	20.7	53.3	55.8	1.2
107	409	64.8	35.2	42.0	45.8	1.0
108	410	65.7	34.3	41.9	44.7	1.1
109	411	60.5	39.2	23.4	26.8	0.8

Appendix Table 1 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
110	413	47.5	52.0	22.7	25.9	0.6
111	414	42.5	57.4	19.9	22.0	0.8
112	416	73.5	26.3	50.1	52.2	1.3
113	417	34.9	64.9	18.3	19.2	0.7
114	420	70.7	29.4	39.0	43.8	0.8
115	423	69.9	29.9	45.9	49.5	1.3
116	424	85.6	14.3	55.5	63.6	1.1
117	427	96.7	8.3	56.1	69.6	1.6
118	428	49.2	50.6	22.0	22.7	0.4
119	430	39.9	59.9	21.1	22.4	1.0
120	431	76.6	23.2	55.3	59.4	1.2
121	432	48.2	51.8	37.3	40.5	0.8
122	433	78.9	20.9	45.5	52.8	1.3
123	435	44.2	55.9	19.9	22.7	0.7
124	436	29.7	70.4	14.9	16.2	0.5
125	437	77.1	23.0	44.7	51.6	1.1
126	439	69.4	30.7	47.0	53.8	1.2
127	440	77.1	23.0	46.8	47.2	1.1
128	441	77.5	22.6	45.9	50.0	1.0
129	443	58.2	42.2	30.8	35.3	0.7
130	444	23.9	76.2	17.8	19.2	0.6
131	445	33.9	66.2	11.8	19.6	0.9
132	446	66.9	33.3	38.3	46.1	1.0
133	447	43.1	56.7	19.1	23.1	0.6
134	449	55.9	43.8	31.5	38.9	1.4
135	452	73.4	26.6	39.6	42.9	0.9
136	454	80.2	21.1	39.8	48.5	1.1
137	455	34.3	65.6	25.3	28.0	0.7
138	459	78.8	21.1	44.2	49.9	0.9

Appendix Table 1 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	YIELDP (g)	GRNPLA[a] (g/dm^2)
139	461	61.5	38.4	30.2	32.1	0.8
140	462	64.7	36.2	36.0	42.2	1.1
141	465	31.6	68.6	17.3	19.7	0.8
142	466	86.1	13.8	62.8	64.8	1.5
143	469	82.6	17.4	43.4	52.0	1.5
144	470	77.5	25.0	67.7	74.3	1.0
Average		64.8	35.5	38.3	42.7	1.0
L.S.D. (.05)		21.7	21.5	17.1	19.1	0.6

Appendix Table 2. PROLIF (prolificacy), BARREN (percent barren plants), YIELD (grain yield), SECOND (second ear grain as a percentage of total grain weight), YIELDP (grain per plant) and GRNPLA (grain per unit leaf area) for 144 random S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm^2)
1	236	84.9	22.3	38.2	4.3	79.4	1.4
2	237	117.4	7.7	53.3	12.5	125.6	2.2
3	239	101.7	11.0	42.7	5.1	91.7	2.2
4	242	82.4	19.9	42.7	2.1	89.4	1.9
5	244	97.6	7.3	43.1	2.1	92.5	1.8
6	245	125.6	5.0	56.4	12.9	113.7	2.6
7	246	72.7	29.8	41.1	0.9	84.9	2.1
8	247	99.6	2.7	45.8	1.1	107.7	2.0
9	248	100.0	7.5	47.5	2.0	98.3	1.8
10	249	80.9	26.4	47.7	4.4	84.6	2.2
11	250	84.3	18.7	35.4	0.6	80.0	1.7
12	253	89.8	10.5	47.8	0.0	100.5	2.0
13	254	84.1	18.4	40.1	2.0	85.7	1.9
14	255	91.7	8.5	51.2	0.5	114.1	2.1
15	257	105.1	2.7	56.9	3.0	127.4	2.2
16	258	89.5	10.5	39.4	0.2	82.2	1.7
17	259	97.5	4.9	38.9	1.1	86.2	1.7
18	260	80.2	19.9	37.1	0.1	75.7	1.7
19	261	90.3	12.6	40.1	3.4	83.9	1.7
20	262	98.2	12.3	47.9	2.4	103.2	2.4
21	265	105.4	5.3	44.9	6.0	94.3	1.8
22	266	81.3	21.3	35.5	0.4	79.6	1.9

[a]Measured in 1974 and 1975.

Appendix Table 2 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm^2)
23	268	62.4	37.8	34.6	0.3	70.0	1.8
24	270	92.2	8.1	55.9	0.4	116.2	2.4
25	272	97.6	7.2	42.3	0.9	91.5	2.1
26	274	97.5	2.6	42.6	0.2	84.2	2.4
27	275	94.9	10.0	57.5	1.7	117.8	2.7
28	276	90.1	9.9	38.3	-0.1	89.8	1.5
29	278	89.8	10.0	47.8	-0.3	98.6	1.8
30	281	84.7	15.2	47.7	-0.2	99.1	2.0
31	282	89.1	11.0	48.8	0.0	107.0	1.9
32	283	89.8	10.2	37.5	-0.1	76.3	1.9
33	284	79.9	20.2	40.6	-0.2	98.4	1.7
34	285	97.3	2.6	58.0	-0.1	125.4	2.3
35	286	79.9	20.1	31.9	-0.0	72.3	1.6
36	287	97.5	5.2	50.3	1.3	104.1	2.2
37	288	84.8	17.4	53.4	0.3	110.2	2.8
38	289	88.2	11.8	33.8	0.2	78.6	1.9
39	291	89.6	10.2	50.0	-0.1	100.0	2.1
40	292	89.7	10.1	51.0	-0.1	106.2	2.0
41	294	82.2	17.5	33.1	-0.3	67.8	1.2
42	295	87.4	14.9	39.1	0.3	81.0	1.9
43	298	92.5	18.5	32.3	6.6	70.7	1.7
44	299	86.7	18.1	34.9	1.0	75.0	1.8
45	300	89.1	10.9	38.7	-0.2	86.1	1.5
46	301	93.5	6.3	50.4	-0.1	108.9	2.2
47	302	57.1	42.9	29.5	-0.0	55.3	1.2
48	305	87.1	12.9	39.9	0.0	84.0	1.6
49	306	92.4	9.8	43.1	0.6	90.7	1.9
50	307	92.3	17.7	38.8	5.3	80.6	1.7
51	310	71.2	31.3	27.6	-0.2	68.5	1.2

Appendix Table 2 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm2)
52	311	102.6	9.9	49.1	5.6	105.0	1.9
53	314	102.1	2.6	45.0	0.3	94.8	2.0
54	315	105.3	-0.2	50.0	0.4	106.3	1.7
55	316	107.6	5.0	50.2	8.1	106.4	2.0
56	318	86.8	13.0	52.7	-0.2	111.7	2.0
57	319	81.2	37.7	36.8	-0.4	81.3	1.4
58	320	96.8	5.4	51.0	0.9	107.4	2.3
59	325	97.7	10.7	31.4	4.1	71.0	1.3
60	326	70.0	40.0	28.7	-0.1	58.8	1.6
61	327	104.7	5.4	41.5	5.6	96.0	2.1
62	328	91.6	8.5	51.0	0.2	120.9	2.5
63	329	92.0	10.4	38.6	1.2	85.3	1.6
64	330	90.4	9.6	44.0	-0.0	92.5	2.0
65	331	97.7	2.5	55.0	-0.3	126.3	2.5
66	336	108.1	4.4	53.3	4.1	114.3	2.2
67	337	95.7	4.4	52.1	0.1	109.0	2.0
68	343	107.6	-0.1	51.4	1.6	111.0	2.0
69	345	108.3	4.6	56.2	2.2	120.1	1.8
70	346	94.9	8.0	38.8	1.2	86.7	2.1
71	347	81.6	21.1	37.4	0.8	82.8	1.8
72	349	85.3	14.9	37.1	0.1	79.8	1.8
73	350	80.1	24.8	33.4	2.7	68.7	1.3
74	351	99.2	11.0	47.1	5.1	100.7	1.9
75	354	85.1	17.6	37.3	1.8	77.8	1.6
76	355	75.5	24.5	27.4	0.0	67.5	1.2
77	356	95.0	12.4	42.1	1.4	85.8	2.1
78	358	110.2	2.3	46.3	2.3	95.6	1.9
79	360	82.5	22.8	32.2	5.3	67.9	2.0
80	361	94.5	8.3	45.0	1.5	99.3	2.2

Appendix Table 2 (Continued)

Entry	S_1 family	PROLIF (ear/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm^2)
81	364	86.7	13.5	47.0	-0.1	101.6	1.8
82	365	97.2	2.7	49.1	-0.0	105.9	1.9
83	369	89.6	10.5	49.8	0.1	104.1	1.8
84	370	87.7	17.5	48.9	2.6	100.3	1.8
85	372	92.4	9.9	48.2	2.4	99.2	1.8
86	373	94.8	5.4	54.8	0.4	127.1	2.1
87	374	60.7	41.7	30.9	0.2	67.2	1.4
88	377	69.1	30.9	26.8	0.1	57.2	1.7
89	378	77.4	22.5	39.0	-0.1	79.5	1.7
90	380	71.8	28.2	36.5	0.0	76.8	2.3
91	381	90.1	15.0	45.6	1.0	98.9	2.1
92	382	82.1	17.9	42.1	0.2	86.7	2.0
93	383	85.0	15.2	38.3	1.2	78.6	1.4
94	384	112.1	5.4	51.7	4.4	108.1	2.0
95	385	104.2	13.4	47.9	7.6	104.3	2.3
96	388	84.0	16.4	36.0	0.3	77.3	1.8
97	389	112.8	7.2	59.8	11.5	123.1	2.2
98	390	90.2	10.1	44.6	0.7	98.8	2.6
99	392	97.6	5.3	47.8	2.2	101.2	2.0
100	396	103.0	13.2	47.2	9.2	103.2	2.0
101	397	101.0	4.8	48.1	4.0	104.2	1.9
102	400	86.9	10.8	39.4	0.3	90.0	1.5
103	401	93.3	9.8	41.1	1.3	86.6	1.9
104	402	76.9	23.2	44.0	0.4	94.9	2.0
105	404	90.4	17.4	37.4	2.6	76.8	1.9
106	408	117.5	2.6	59.8	7.1	123.0	2.5
107	409	79.1	21.2	46.7	0.5	101.5	1.9
108	410	84.9	15.5	43.6	0.5	94.0	1.8
109	411	87.7	14.7	41.4	0.2	85.6	1.5

Appendix Table 2 (Continued)

Entry	S_1 family	PROLIF (ears/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm^2)
110	413	87.1	15.6	36.4	0.9	78.8	1.3
111	414	81.0	21.5	33.8	1.3	74.1	1.5
112	416	95.2	9.9	50.0	2.8	104.4	2.3
113	417	90.2	12.3	41.4	1.0	85.2	2.4
114	420	87.9	12.2	43.1	0.0	89.7	2.0
115	423	87.5	12.7	45.8	0.3	96.8	2.1
116	424	102.1	5.7	46.6	3.3	102.6	2.0
117	427	111.1	4.9	48.8	5.3	106.5	2.3
118	428	94.9	5.1	37.0	0.1	81.0	2.0
119	430	74.3	25.9	34.4	0.2	72.7	1.8
120	431	97.9	4.9	49.2	2.4	101.7	2.2
121	432	89.3	13.0	47.9	1.9	100.6	1.7
122	433	97.4	2.7	46.0	0.2	95.3	2.3
123	435	76.8	23.1	34.3	0.0	71.4	1.0
124	436	67.0	33.0	24.6	-0.0	52.7	1.4
125	437	107.2	5.6	45.1	5.7	98.9	2.1
126	439	100.1	9.8	48.5	5.2	105.7	2.6
127	440	97.7	2.3	53.5	0.1	110.3	1.9
128	441	94.2	5.8	48.9	-0.0	102.4	1.9
129	443	79.6	20.5	37.9	-0.1	80.8	1.4
130	444	75.7	24.2	32.5	-0.1	70.3	2.1
131	445	65.6	34.5	21.0	0.0	50.7	1.3
132	446	103.4	7.5	54.6	4.6	114.4	2.1
133	447	97.4	4.9	40.0	-0.0	83.4	1.4
134	449	86.0	19.8	31.9	3.5	74.8	1.3
135	452	97.2	2.7	45.3	-0.2	96.9	1.7
136	454	113.1	5.0	53.2	8.2	114.2	2.1
137	455	74.3	25.5	38.0	-0.5	80.0	1.4
138	459	97.5	7.4	49.4	2.8	102.7	2.1

Appendix Table 2 (Continued)

Entry	S_1 family	PROLIF (ear/100 pl)	BARREN (%)	YIELD (q/ha)	SECOND (%)	YIELDP (g)	GRNPLA[a] (g/dm^2)
139	461	92.1	7.9	38.6	-0.1	82.3	1.9
140	462	97.3	12.8	49.5	4.9	106.2	1.9
141	465	82.5	17.6	41.6	-0.3	86.5	2.0
142	466	99.5	2.8	54.7	1.7	133.3	2.5
143	469	96.9	11.1	42.7	2.6	92.2	2.3
144	470	110.2	7.6	65.2	12.3	138.2	1.9
Average		91.2	13.2	43.5	1.9	93.0	1.9
L.S.D. (.05)		22.9	19.3	15.8	5.7	34.7	0.9

Appendix Table 3. Days from July 1 to 25, 50 and 75% anthesis and silk emergence, respectively, PSS (days from 50% anthesis to 50% silk emergence), SI (days from 25% to 75% silk emergence) and SD (days from anthesis to silk emergence of the same plant) for 144 random S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

		Anthesis			Silk Emergence					
Entry	S_1 family	25%	50%	75%	25%	50%	75%	PSS	SI	SD
1	236	23.8	26.6	28.6	26.8	31.0	38.0	4.2	11.4	6.1
2	237	21.7	23.8	25.3	26.1	29.6	31.9	5.5	6.1	5.6
3	239	21.3	23.5	24.8	25.6	27.7	29.7	4.2	4.4	4.9
4	242	25.3	27.6	28.9	30.0	34.7	43.2	7.1	13.5	9.0
5	244	19.1	21.6	22.4	22.1	24.5	25.4	2.8	3.5	3.2
6	245	20.3	22.4	23.9	22.1	25.4	27.1	2.8	5.1	3.3
7	246	21.0	22.9	24.4	31.4	34.4	39.0	11.4	7.4	12.0
8	247	17.5	19.7	21.0	20.5	22.1	25.3	2.2	4.9	4.0
9	248	25.4	27.5	29.2	29.8	33.6	37.7	5.8	8.3	6.5
10	249	21.7	23.8	25.2	25.6	28.6	30.8	4.6	5.6	5.2
11	250	22.4	24.1	25.3	25.2	28.9	33.2	4.7	8.1	6.1
12	253	21.8	24.3	25.8	26.7	30.3	32.9	5.8	6.3	6.5
13	254	26.1	27.6	28.4	31.0	34.6	41.0	7.1	10.0	7.8
14	255	20.3	21.8	23.6	22.0	23.4	25.5	1.6	3.6	2.1
15	257	21.6	23.4	25.1	25.6	28.0	30.2	4.8	4.8	4.7
16	258	18.0	20.1	21.1	22.2	23.3	27.4	3.3	5.4	5.3
17	259	23.9	25.8	27.6	27.5	29.6	32.2	3.9	4.8	4.5
18	260	25.6	26.7	29.0	27.1	31.2	36.1	4.6	9.1	5.8
19	261	20.4	22.3	24.6	25.0	27.9	31.3	5.9	6.0	6.9
20	262	21.0	22.8	24.8	22.9	25.4	27.5	2.7	4.6	2.4
21	265	24.4	26.8	27.7	29.8	31.7	34.6	4.8	4.9	6.6
22	266	23.5	25.5	27.0	25.5	29.0	31.9	3.6	6.6	4.9
23	268	25.5	28.0	29.1	30.3	36.8	41.3	9.2	11.0	8.3
24	270	23.6	26.2	28.1	25.9	29.0	31.5	2.8	5.5	3.7

Appendix Table 3 (Continued)

		Anthesis			Silk Emergence					
Entry	S_1 family	25%	50%	75%	25%	50%	75%	PSS	SI	SD
25	272	25.1	27.0	29.7	28.2	30.2	32.0	3.1	3.8	2.5
26	274	23.5	24.6	26.7	27.1	29.8	32.0	4.7	4.9	4.3
27	275	22.3	24.6	27.1	23.5	27.1	30.0	2.5	6.4	2.6
28	276	19.9	22.6	24.4	25.8	30.3	35.7	5.4	9.9	9.4
29	278	21.2	22.8	24.6	25.0	27.7	30.9	4.7	5.9	6.2
30	281	22.2	24.9	27.9	26.4	28.6	30.7	3.5	4.1	3.9
31	282	20.6	22.6	23.7	23.9	26.7	30.5	4.1	6.1	5.4
32	283	21.2	22.9	25.6	24.2	27.7	31.5	4.5	7.1	4.7
33	284	21.9	24.4	27.8	27.7	33.6	37.3	8.9	9.6	8.6
34	285	23.5	25.8	27.9	26.6	29.2	33.2	3.2	6.8	5.4
35	286	22.5	24.4	26.0	27.7	29.3	33.0	4.8	5.3	6.4
36	287	19.4	21.3	22.2	23.0	25.3	27.5	3.8	4.3	4.8
37	288	21.5	22.7	24.5	27.6	29.8	33.0	7.2	5.3	8.0
38	289	23.0	25.3	27.7	27.7	29.8	33.4	4.5	5.8	5.6
39	291	22.4	24.4	25.5	24.3	27.1	35.4	2.9	11.1	6.1
40	292	25.3	27.0	28.4	31.0	36.8	40.8	10.2	9.8	9.7
41	294	21.7	24.4	27.5	26.6	31.7	40.9	7.4	14.3	9.6
42	295	20.8	22.5	23.4	24.5	27.7	30.5	5.3	5.9	6.8
43	298	24.2	26.8	28.9	28.7	34.1	40.4	7.5	11.3	8.1
44	299	24.3	27.0	29.5	30.2	38.9	42.5	11.9	12.1	9.3
45	300	23.6	25.5	26.9	28.7	30.9	32.8	5.4	4.1	6.0
46	301	22.2	24.3	25.6	28.0	29.4	32.3	5.2	4.5	6.3
47	302	20.5	21.8	23.6	26.0	30.5	39.6	8.9	13.5	11.1
48	305	24.2	26.6	28.6	30.7	35.8	41.5	9.2	10.5	9.8
49	306	22.3	24.2	24.9	27.9	31.1	36.3	7.0	8.4	8.9
50	307	23.7	25.4	26.9	25.4	28.4	30.5	2.9	5.3	10.4
51	310	24.1	25.9	27.3	29.8	33.9	39.2	8.2	9.5	8.9

Appendix Table 3 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
52	311	23.3	25.4	26.8	26.0	29.1	31.2	3.9	5.4	3.8
53	314	26.1	27.1	28.2	29.7	31.8	35.1	4.7	5.5	6.5
54	315	18.0	20.5	21.7	22.5	24.1	27.1	3.7	4.6	3.8
55	316	23.4	26.3	27.3	25.9	30.1	35.9	4.0	9.6	6.3
56	318	22.2	23.6	25.3	26.0	28.6	31.0	5.0	5.0	6.2
57	319	24.0	26.0	28.5	30.5	37.9	42.0	11.8	11.6	10.6
58	320	24.8	26.8	28.0	28.3	30.8	33.3	4.1	5.3	5.6
59	325	21.1	23.2	24.8	26.1	28.1	30.9	5.1	4.9	6.4
60	326	21.6	24.6	27.0	28.9	33.2	36.4	8.6	7.4	8.7
61	327	25.3	27.4	28.6	30.0	34.2	37.1	6.8	7.0	6.6
62	328	24.7	26.1	27.3	27.6	31.8	35.5	5.6	7.9	6.9
63	329	19.6	21.4	23.8	21.2	24.3	26.6	3.0	5.3	3.1
64	330	19.5	21.6	23.4	26.1	28.7	32.2	7.2	6.0	8.4
65	331	22.8	24.7	26.6	25.7	27.8	29.4	3.1	3.6	3.0
66	336	24.3	25.8	26.6	26.9	29.4	32.9	3.7	5.9	4.7
67	337	15.5	17.3	18.9	19.2	21.3	23.8	4.1	4.1	5.0
68	343	21.4	22.8	24.4	22.2	24.4	27.4	1.5	5.0	1.1
69	345	23.9	25.2	27.0	28.9	31.9	37.6	6.5	8.6	7.2
70	346	21.5	23.2	24.7	23.4	25.9	29.9	2.7	6.5	4.0
71	347	21.0	22.6	23.4	25.7	29.9	33.9	7.4	8.0	8.4
72	349	24.1	26.0	28.2	28.5	32.2	38.1	6.2	9.4	7.4
73	350	20.7	22.0	22.5	24.9	25.7	34.0	3.8	9.0	7.8
74	351	23.8	25.6	27.2	27.9	29.9	32.3	4.3	4.5	4.9
75	354	24.8	26.6	27.7	29.9	33.2	37.3	6.8	7.4	8.2
76	355	24.1	26.1	27.3	29.2	33.7	37.3	7.8	8.1	8.4
77	356	24.8	26.7	28.2	30.8	35.0	40.9	8.3	10.1	9.9
78	358	24.2	25.8	27.9	27.0	29.2	31.5	3.5	4.4	4.1

Appendix Table 3 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
79	360	25.4	26.3	27.5	28.4	31.7	39.4	5.5	10.5	8.3
80	361	22.9	24.8	25.8	25.7	28.6	31.3	3.9	5.4	4.8
81	364	23.4	24.8	25.7	25.7	28.7	33.3	3.8	7.6	5.9
82	365	19.7	21.6	22.2	24.7	27.0	29.0	5.5	4.4	7.7
83	369	19.3	21.3	22.6	24.4	25.7	30.7	4.5	6.1	6.3
84	370	23.5	25.9	28.7	26.6	31.4	34.7	5.5	7.8	5.8
85	372	21.8	23.1	25.3	26.6	29.0	36.1	5.9	9.5	8.0
86	373	23.5	25.9	28.0	26.2	30.3	34.9	4.1	8.9	5.7
87	374	22.2	24.6	25.4	29.7	36.3	43.1	11.6	13.4	11.8
88	377	23.9	25.8	27.6	28.3	37.9	44.8	11.9	16.5	10.5
89	378	22.2	24.4	26.7	27.2	32.7	35.4	8.1	8.3	8.2
90	380	24.0	26.0	27.4	28.1	31.5	36.6	5.4	8.5	7.2
91	381	24.4	26.2	28.0	31.7	37.5	41.6	11.2	9.5	10.8
92	382	22.7	23.7	25.6	26.1	29.1	30.8	5.2	4.6	5.7
93	383	22.6	25.2	26.6	26.6	32.8	40.0	7.2	13.5	8.6
94	384	22.4	24.8	26.3	26.8	30.5	33.8	5.6	7.3	6.6
95	385	24.1	26.0	27.2	25.1	27.6	29.4	1.5	4.3	2.1
96	388	25.0	26.6	27.8	28.7	30.7	33.0	3.9	4.1	5.6
97	389	23.2	24.6	26.1	24.6	25.9	28.2	1.5	3.6	1.8
98	390	18.1	20.4	22.6	20.9	24.8	26.4	4.4	5.6	4.8
99	392	21.1	22.8	24.0	23.5	26.1	28.7	3.5	5.4	4.7
100	396	24.5	26.5	28.2	29.4	32.2	34.6	5.8	5.4	6.5
101	397	27.8	29.7	31.2	30.2	32.6	35.7	3.0	5.6	4.3
102	400	26.1	28.8	29.8	31.0	38.9	41.8	10.3	10.9	9.0
103	401	20.4	21.9	23.4	23.8	26.0	30.4	4.4	6.4	6.3
104	402	20.8	22.5	24.8	26.4	29.1	34.5	6.7	8.1	8.0
105	404	20.5	22.6	24.0	25.4	29.1	37.0	6.4	11.8	9.2

Appendix Table 3 (Continued)

		Anthesis			Silk Emergence					
Entry	S_1 family	25%	50%	75%	25%	50%	75%	PSS	SI	SD
106	408	23.6	25.4	27.3	25.3	27.4	30.1	2.2	5.1	2.5
107	409	22.7	25.3	27.5	28.6	30.7	37.9	5.6	9.4	7.6
108	410	22.0	23.9	26.0	25.1	28.4	32.6	4.6	7.4	6.2
109	411	25.4	27.1	29.4	31.0	36.2	41.5	9.3	10.5	8.7
110	413	28.7	29.9	31.2	35.1	37.9	40.9	8.6	6.0	8.5
111	414	23.0	24.4	25.2	27.1	30.0	36.0	5.8	8.9	7.6
112	416	24.7	27.3	28.5	28.5	30.8	36.0	3.8	7.6	4.9
113	417	24.4	26.6	28.6	34.3	39.6	44.9	10.6	10.6	12.3
114	420	20.8	22.5	24.6	23.2	25.2	29.1	2.9	5.9	3.5
115	423	23.7	26.6	28.1	28.4	32.2	37.8	5.8	9.0	7.6
116	424	21.4	23.1	24.5	25.1	27.5	29.7	4.5	4.6	3.9
117	427	21.2	22.6	24.4	21.6	23.2	24.7	0.6	3.1	1.3
118	428	24.1	25.9	26.8	29.5	34.8	39.1	9.5	9.8	9.0
119	430	25.2	26.8	27.8	29.6	39.2	45.4	12.6	15.8	10.9
120	431	23.3	25.6	26.0	25.2	27.4	29.3	1.9	3.9	3.0
121	432	20.1	22.7	24.0	21.9	29.9	36.0	7.2	14.1	8.2
122	433	19.5	20.7	22.6	21.5	23.9	26.0	3.1	4.6	3.5
123	435	23.4	25.8	26.6	27.7	30.2	38.0	4.5	10.4	7.1
124	436	26.0	27.6	29.9	35.2	39.4	44.5	11.8	11.9	10.8
125	437	21.7	23.6	25.0	23.5	25.8	26.7	2.1	3.3	2.5
126	439	24.5	26.8	28.2	28.5	31.7	35.1	4.8	6.6	5.5
127	440	20.4	23.7	25.9	25.1	27.7	30.6	4.0	5.1	4.6
128	441	21.0	23.1	24.8	22.6	25.1	27.6	1.9	5.0	2.7
129	443	23.1	25.2	27.5	30.0	37.3	41.6	11.9	11.8	10.8
130	444	24.8	27.4	29.1	29.9	37.8	43.1	10.3	13.6	10.0
131	445	27.3	30.0	32.1	32.4	42.0	44.3	12.0	11.9	8.5
132	446	22.4	24.1	25.9	25.4	27.9	33.4	3.7	7.9	5.8

Appendix Table 3 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
133	447	23.1	24.7	25.3	32.6	36.2	43.9	11.5	11.5	12.6
134	449	21.3	22.8	25.3	24.5	27.1	37.4	4.1	11.6	7.8
135	452	23.8	25.7	27.6	27.2	30.6	34.1	5.0	7.1	5.3
136	454	23.6	24.8	28.3	26.1	29.7	33.1	4.9	7.3	4.5
137	455	23.4	25.2	27.5	27.4	32.7	37.6	8.0	10.4	7.9
138	459	22.8	24.4	26.5	24.2	26.2	28.2	1.8	4.1	2.0
139	461	21.1	22.9	24.8	24.5	27.1	31.2	4.2	6.4	5.3
140	462	25.1	27.9	30.2	27.9	29.9	35.9	1.9	8.1	4.4
141	465	25.4	27.4	29.1	29.5	34.9	40.6	7.3	11.4	7.9
142	466	25.6	27.4	29.6	26.8	31.7	33.9	4.2	5.3	4.4
143	469	21.2	24.2	26.3	23.3	25.8	31.1	1.6	7.9	3.1
144	470	22.1	24.6	26.2	25.4	27.5	30.1	2.8	4.6	4.1
Average		22.7	24.7	26.4	26.8	30.3	34.3	5.5	7.5	6.4
L.S.D. (.05)		1.8	2.0	2.3	2.8	4.5	6.3	4.2	5.4	3.7

Appendix Table 4. Days from July 1 to 25, 50 and 75% anthesis and silk emergence, respectively, PSS (days from 50% anthesis to 50% silk emergence), SI (days from 25% to 75% silk emergence) and SD (days from anthesis to silk emergence of the same plant) for 144 random S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

		Anthesis			Silk Emergence					
Entry	S_1 family	25%	50%	75%	25%	50%	75%	PSS	SI	SD
1	236	23.4	24.9	26.3	24.8	27.7	31.8	2.9	6.5	3.5
2	237	20.6	21.8	23.6	23.2	25.8	28.0	4.1	4.8	3.9
3	239	20.1	22.0	24.5	22.0	24.0	26.8	2.0	4.9	3.4
4	242	24.8	25.7	27.3	27.8	29.1	35.6	3.5	7.8	5.2
5	244	19.6	21.3	22.7	20.3	22.2	25.6	1.0	5.2	2.1
6	245	19.1	20.8	21.9	21.0	21.9	23.9	1.9	3.1	1.7
7	246	20.4	22.2	24.6	26.3	29.7	35.6	7.5	8.8	8.6
8	247	16.7	18.3	20.2	19.3	20.7	22.6	2.3	3.5	3.0
9	248	26.2	27.5	28.6	30.0	32.2	35.1	4.7	5.4	4.9
10	249	21.8	23.6	24.7	23.5	25.9	28.4	2.3	4.8	3.6
11	250	21.2	23.0	25.1	21.8	24.5	28.4	1.4	7.1	2.9
12	253	22.2	23.6	24.8	25.1	27.4	29.9	3.9	4.8	4.9
13	254	23.6	25.8	26.8	27.0	29.6	33.6	3.9	6.1	5.2
14	255	19.5	23.0	24.0	19.6	23.9	25.9	1.0	6.2	1.7
15	257	21.1	22.8	24.9	24.7	26.2	28.1	3.4	3.5	3.1
16	258	17.5	19.2	20.0	19.1	21.4	23.8	2.2	4.5	3.6
17	259	22.2	24.2	26.0	24.6	26.9	28.4	2.7	3.5	2.3
18	260	22.1	23.6	25.3	23.1	25.3	28.5	1.6	5.6	2.2
19	261	20.2	21.4	22.6	22.1	23.5	27.9	2.2	5.0	3.4
20	262	21.2	23.2	24.6	22.6	24.0	25.6	0.7	3.1	1.4
21	265	23.4	25.6	27.3	27.5	29.5	30.3	3.8	3.0	4.0
22	266	21.7	24.6	26.3	24.1	26.1	28.6	1.8	4.4	1.9
23	268	24.8	26.3	27.4	27.7	30.6	37.9	4.1	10.6	6.0
24	270	22.5	24.4	26.4	23.4	25.3	28.9	0.9	5.4	1.5

Appendix Table 4 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
25	272	24.7	26.5	28.8	26.4	28.4	31.6	1.9	5.1	2.3
26	274	21.8	24.9	26.7	24.8	28.0	31.8	3.1	7.3	4.1
27	275	21.8	23.8	25.4	22.3	24.2	26.5	0.2	4.7	1.3
28	276	17.9	21.2	22.4	24.0	26.0	29.8	4.7	6.0	5.8
29	278	20.1	22.4	24.2	23.5	26.3	28.6	3.8	5.3	4.2
30	281	21.9	24.1	25.4	23.3	26.4	28.6	2.1	5.8	2.5
31	282	21.0	22.3	24.8	23.3	25.5	26.8	3.1	3.2	2.4
32	283	20.3	21.8	23.7	23.2	25.5	27.1	2.8	4.3	3.3
33	284	20.4	24.1	28.0	25.6	28.3	30.9	4.0	5.9	5.4
34	285	22.2	23.7	25.9	24.2	26.2	28.1	2.4	4.1	2.8
35	286	21.4	22.1	23.7	25.3	27.8	29.4	5.7	4.9	6.9
36	287	19.7	20.5	21.7	22.1	23.7	24.5	3.0	2.6	2.5
37	288	21.1	23.1	24.9	26.8	29.7	32.1	6.6	5.3	6.1
38	289	22.2	23.5	25.6	24.8	27.2	31.1	3.6	6.6	4.3
39	291	21.4	23.1	24.4	22.9	24.4	27.8	1.1	5.3	2.5
40	292	23.8	25.7	27.6	28.8	30.9	32.3	5.1	3.8	4.7
41	294	21.2	22.9	26.1	24.6	28.6	33.3	5.6	11.4	6.2
42	295	20.8	21.9	23.1	22.6	25.1	28.8	3.0	6.7	4.4
43	298	24.8	26.2	28.1	28.4	30.7	33.5	4.3	4.8	4.5
44	299	24.0	26.2	28.9	28.0	31.1	33.1	4.7	5.6	4.3
45	300	22.6	23.5	26.4	26.0	28.5	30.9	4.8	5.5	4.4
46	301	21.6	22.6	24.5	24.0	26.9	29.4	3.4	5.6	4.1
47	302	20.3	21.0	22.1	23.8	27.0	32.8	5.7	12.3	9.3
48	305	22.6	24.6	26.3	28.0	30.1	31.6	5.4	3.9	6.3
49	306	21.4	23.4	24.9	24.4	26.8	29.1	3.5	4.5	4.4
50	307	22.9	24.5	25.3	24.1	25.7	28.0	1.2	4.1	2.1
51	310	22.7	24.7	26.7	26.9	31.1	37.8	6.4	11.2	7.6

Appendix Table 4 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
52	311	22.0	23.6	25.7	24.0	26.0	28.3	2.5	4.3	2.0
53	314	25.2	26.5	27.8	27.9	29.4	31.9	3.1	4.0	4.0
54	315	18.3	19.7	20.8	20.4	22.4	23.3	2.7	3.3	2.4
55	316	21.9	24.6	25.8	23.4	26.8	30.5	2.2	6.6	2.9
56	318	21.5	23.7	24.6	26.1	27.3	28.5	3.5	2.6	3.9
57	319	23.0	24.8	25.6	26.1	28.5	32.3	3.7	6.6	5.5
58	320	23.8	25.3	26.9	26.2	28.2	31.0	2.9	4.8	2.9
59	325	21.1	22.3	23.8	24.0	26.0	27.8	3.5	4.4	3.8
60	326	22.0	24.2	26.1	26.9	29.5	30.8	5.4	4.0	6.3
61	327	25.5	27.6	28.7	29.7	33.0	35.0	5.5	5.1	5.6
62	328	23.3	24.2	25.8	23.6	26.1	28.3	2.0	4.8	2.1
63	329	20.0	21.7	23.1	20.3	22.6	24.0	0.9	4.0	1.6
64	330	19.2	20.5	22.6	22.8	26.3	28.8	5.9	6.1	6.3
65	331	21.1	23.1	24.5	23.6	25.2	27.0	2.2	3.5	3.0
66	336	23.6	24.4	26.3	24.6	27.9	29.3	3.5	5.0	3.6
67	337	15.9	17.0	18.2	17.7	19.7	21.3	2.7	3.1	3.5
68	343	20.3	22.1	24.0	20.5	22.2	24.0	0.0	3.8	0.6
69	345	22.7	24.8	26.5	25.2	28.7	31.1	3.9	6.4	4.9
70	346	21.0	22.9	24.5	22.1	24.7	28.8	1.9	6.7	2.9
71	347	21.2	22.5	23.6	24.2	27.0	29.8	4.4	6.2	6.0
72	349	23.5	25.5	26.7	26.6	28.5	31.9	3.0	5.5	4.1
73	350	19.1	21.1	23.3	21.6	23.3	26.5	2.3	4.4	3.9
74	351	23.0	24.2	26.1	25.1	27.0	31.6	2.9	6.4	4.2
75	354	23.7	25.0	27.0	26.8	28.8	34.8	3.8	7.4	6.4
76	355	23.6	25.0	27.0	26.3	28.6	31.9	3.7	5.4	4.5
77	356	23.4	25.6	26.4	27.0	30.1	32.6	4.7	5.4	4.6
78	358	23.9	26.0	27.2	27.1	29.0	30.5	3.0	3.4	3.3

Appendix Table 4 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
79	360	25.2	26.6	28.0	27.5	29.7	32.9	3.2	4.6	4.4
80	361	22.1	24.4	26.2	23.9	26.0	29.9	1.6	5.9	3.7
81	364	21.3	23.3	24.6	22.7	24.1	26.4	0.9	3.8	1.6
82	365	19.0	20.9	22.1	21.6	23.1	25.0	2.2	3.1	2.8
83	369	19.0	20.7	22.4	21.1	24.8	26.6	4.0	5.9	4.6
84	370	22.6	24.4	26.1	24.6	27.9	33.1	3.6	8.4	4.3
85	372	20.4	23.0	24.8	23.1	26.0	27.9	3.1	4.4	3.6
86	373	23.1	26.6	28.0	24.4	28.0	30.0	1.6	5.8	2.2
87	374	20.5	22.9	24.9	26.2	29.7	36.9	6.8	10.8	8.4
88	377	23.1	25.1	26.7	27.7	29.7	36.1	4.7	8.4	7.1
89	378	21.8	24.5	26.2	26.6	29.5	32.0	5.0	5.3	5.8
90	380	21.9	24.3	25.4	25.8	28.6	30.4	4.2	4.8	5.2
91	381	23.4	25.6	26.8	28.3	31.6	35.8	6.2	7.0	7.0
92	382	22.1	23.6	25.7	23.9	26.9	29.3	3.2	5.4	3.5
93	383	21.5	23.8	25.6	24.6	27.4	29.1	3.6	4.8	4.5
94	384	22.1	23.5	25.2	24.3	26.6	29.1	3.1	4.7	3.7
95	385	22.5	24.0	25.3	22.4	24.0	25.9	0.6	4.0	0.1
96	388	22.8	25.4	26.9	24.9	27.7	32.5	2.3	7.6	4.4
97	389	22.2	23.9	25.3	22.3	24.3	26.1	1.0	3.5	0.6
98	390	16.9	18.4	20.4	17.2	19.3	20.8	1.1	3.9	0.7
99	392	20.2	21.6	22.8	22.1	23.5	27.9	2.0	6.0	4.1
100	396	22.9	23.7	24.8	25.0	26.7	28.8	3.1	3.8	3.6
101	397	28.3	28.8	29.7	28.1	30.8	32.8	2.1	4.6	2.4
102	400	26.0	28.1	30.0	28.4	31.9	35.9	3.8	7.8	4.8
103	401	20.4	21.1	23.1	21.0	23.2	25.8	2.2	4.3	2.5
104	402	19.3	21.6	23.1	23.6	25.0	32.0	3.5	8.6	6.1
105	404	20.1	22.1	23.6	22.5	25.0	32.3	2.9	10.1	4.9

Appendix Table 4 (Continued)

Entry	S_1 family	Anthesis 25%	50%	75%	Silk Emergence 25%	50%	75%	PSS	SI	SD
106	408	22.2	23.6	24.7	23.2	24.3	26.1	0.8	3.0	1.1
107	409	22.0	23.8	25.0	24.7	28.2	30.4	4.3	6.3	4.7
108	410	21.2	22.4	27.3	24.2	25.7	28.8	3.4	4.6	3.3
109	411	25.1	26.5	28.5	28.6	31.1	34.0	4.7	4.8	5.1
110	413	27.3	28.3	30.8	30.1	31.6	34.9	3.5	4.5	4.7
111	414	21.0	22.6	24.8	24.3	26.1	30.4	3.6	6.0	5.8
112	416	24.6	25.7	27.3	26.4	28.5	31.0	3.0	4.3	3.4
113	417	23.1	25.7	26.4	28.7	32.2	35.9	6.7	6.8	8.0
114	420	19.8	21.4	23.2	20.5	22.5	26.1	1.1	5.6	2.6
115	423	23.2	25.6	27.5	27.4	30.3	33.1	4.8	5.1	5.6
116	424	20.8	22.6	25.6	23.4	25.5	28.4	2.9	4.8	3.2
117	427	20.9	22.1	24.4	20.4	21.5	23.9	-0.6	3.5	0.1
118	428	22.2	24.1	25.7	26.1	27.5	30.8	3.5	4.4	4.8
119	430	24.0	25.4	26.5	27.1	29.4	41.6	3.9	14.8	7.5
120	431	22.1	23.1	24.6	23.1	25.0	26.5	2.0	3.2	1.8
121	432	21.3	22.8	24.0	25.4	28.2	30.9	5.5	4.8	6.7
122	433	19.4	20.8	21.4	20.6	22.5	24.6	1.8	3.8	2.1
123	435	22.3	24.7	26.5	25.0	28.2	33.3	3.5	8.1	4.9
124	436	25.3	27.5	29.3	30.1	36.6	38.9	9.1	8.4	8.0
125	437	21.6	22.3	23.2	22.2	23.4	25.3	1.2	2.7	1.3
126	439	22.4	24.0	26.0	24.8	27.8	30.3	3.7	5.5	3.2
127	440	20.8	23.1	24.7	24.1	26.6	29.5	3.6	4.6	3.5
128	441	19.5	21.1	22.6	20.5	21.7	23.1	0.5	2.5	1.2
129	443	22.0	24.3	25.9	26.3	29.4	34.0	5.1	7.8	7.2
130	444	24.7	26.3	28.9	28.4	30.3	37.8	4.0	9.1	6.3
131	445	25.6	27.6	30.6	29.2	33.7	38.9	6.0	10.0	6.8
132	446	19.9	22.1	23.1	21.7	24.3	27.6	2.2	5.7	3.1

Appendix Table 4 (Continued)

Entry	S_1 family	Anthesis 25%	Anthesis 50%	Anthesis 75%	Silk Emergence 25%	Silk Emergence 50%	Silk Emergence 75%	PSS	SI	SD
133	447	22.6	24.5	25.4	27.1	29.0	33.4	4.6	5.6	6.6
134	449	20.1	21.8	23.7	22.1	25.0	28.0	3.2	5.6	3.8
135	452	23.3	24.8	26.3	25.7	27.1	30.6	2.4	4.8	3.6
136	454	23.1	25.2	26.6	23.7	26.7	28.9	1.5	4.8	1.8
137	455	22.7	24.6	25.8	23.4	25.3	29.4	0.7	5.6	3.1
138	459	20.7	22.6	24.4	21.8	24.0	25.6	1.4	3.7	1.3
139	461	21.4	22.9	23.6	22.1	25.8	27.9	3.0	4.8	3.2
140	462	24.5	26.1	27.3	27.0	28.5	31.8	2.3	4.5	2.8
141	465	25.3	26.4	27.4	26.3	28.6	29.8	2.2	3.4	2.1
142	466	23.7	26.5	27.4	26.9	29.8	32.1	3.3	4.8	3.6
143	469	20.6	22.1	24.0	21.5	23.4	26.1	1.1	4.9	1.2
144	470	20.8	21.7	23.6	22.0	23.9	26.8	2.1	4.4	3.0
Average		21.9	23.7	25.3	24.5	26.9	29.9	3.2	5.5	3.9
L.S.D. (.05)		1.9	1.8	2.1	2.5	3.1	4.9	2.8	3.9	2.6

Appendix Table 5. ERHT (ear height), PTHT (plant height), ERHT:PTHT (ear-height-to-plant-height ratio), TBN (tassel branch number), PLA (leaf area per plant) and LODG (percent lodged plants) for 144 S_1 families from BSUL1 grown at 96,875 pl/ha in 1975 and 1976

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
1	236	71.9	152.9	0.46	12.7	5638	9.0
2	237	81.6	168.7	0.48	19.5	5440	18.3
3	239	72.8	150.7	0.48	14.4	5061	6.2
4	242	84.1	173.0	0.47	12.8	4907	13.8
5	244	72.1	152.0	0.46	13.4	5241	11.7
6	245	79.2	162.6	0.48	10.0	4885	34.5
7	246	75.4	160.3	0.45	16.9	5114	8.0
8	247	59.3	145.7	0.44	13.4	4691	17.5
9	248	72.3	161.7	0.44	14.8	5700	18.3
10	249	87.1	162.5	0.53	14.6	5628	18.0
11	250	76.6	171.0	0.43	16.4	5140	10.7
12	253	80.1	177.7	0.45	15.6	5988	49.2
13	254	85.7	172.4	0.49	22.2	5253	21.0
14	255	72.4	144.2	0.49	10.3	4985	18.5
15	257	87.7	159.0	0.55	18.9	5273	38.5
16	258	67.9	150.5	0.44	12.3	4858	6.8
17	259	77.3	165.7	0.45	17.7	4946	40.2
18	260	80.9	176.9	0.45	18.0	5582	17.8
19	261	72.3	157.1	0.45	16.9	4952	8.8
20	262	75.0	161.2	0.46	15.9	5142	16.0
21	265	72.5	153.5	0.46	17.3	5486	10.0
22	266	69.2	145.0	0.48	16.8	5115	15.5
23	268	85.7	167.0	0.50	15.9	5262	10.2
24	270	69.8	149.0	0.47	9.9	5550	24.7
25	272	91.2	187.4	0.48	10.4	5768	59.0

[a]Measured in 1974 and 1975.

Appendix Table 5 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
26	274	73.6	159.0	0.45	19.5	5576	19.5
27	275	84.6	160.7	0.52	18.0	5799	25.5
28	276	72.6	157.8	0.45	13.0	5190	3.0
29	278	70.2	158.5	0.43	15.6	5148	26.9
30	281	76.5	144.1	0.53	11.2	5847	36.7
31	282	64.7	162.9	0.38	11.4	5146	28.2
32	283	65.6	153.7	0.41	7.6	4829	23.2
33	284	85.6	169.8	0.49	23.5	4865	7.2
34	285	84.2	175.3	0.48	18.5	5093	18.0
35	286	70.2	167.0	0.41	18.8	5543	10.9
36	287	74.9	167.5	0.44	12.3	5107	27.4
37	288	79.8	171.6	0.46	20.4	5656	17.8
38	289	82.2	164.9	0.49	21.5	5128	19.0
39	291	76.0	154.7	0.49	14.3	5981	28.7
40	292	80.2	159.9	0.51	16.0	4883	5.5
41	294	68.6	151.9	0.44	19.4	5435	13.7
42	295	78.4	158.8	0.49	21.0	4792	6.5
43	298	68.5	146.8	0.47	13.1	5560	1.0
44	299	73.2	156.9	0.47	21.1	5305	34.7
45	300	85.2	176.7	0.48	18.5	5124	27.2
46	301	72.0	161.9	0.44	19.0	5798	7.7
47	302	68.7	162.2	0.42	12.1	4946	22.7
48	305	79.8	162.9	0.49	18.8	5927	23.7
49	306	71.1	152.9	0.45	18.9	5519	18.3
50	307	72.5	147.2	0.48	7.7	5502	12.1
51	310	84.1	177.3	0.46	23.5	6039	12.3
52	311	84.8	183.3	0.43	21.5	5144	27.6

Appendix Table 5 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
53	314	70.4	157.8	0.43	23.3	5120	32.2
54	315	65.0	145.9	0.44	17.2	5154	24.6
55	316	94.3	178.4	0.52	22.4	5062	32.8
56	318	70.5	148.0	0.47	16.4	5994	10.3
57	319	73.3	150.3	0.47	16.7	5616	8.6
58	320	77.6	166.3	0.46	12.2	5248	18.8
59	325	67.8	139.8	0.47	18.8	4968	31.5
60	326	61.9	135.7	0.44	23.5	5594	5.8
61	327	100.1	187.5	52.8	14.5	5187	42.3
62	328	87.0	193.6	0.44	21.6	5180	13.1
63	329	77.3	149.1	0.52	12.9	5627	32.3
64	330	72.3	167.6	0.42	14.4	4930	12.3
65	331	78.1	169.4	0.45	4.8	5544	12.0
66	336	79.2	161.2	0.49	15.1	5286	28.6
67	337	66.1	142.5	0.45	16.0	4525	3.1
68	343	76.3	155.1	0.48	17.8	4898	70.0
69	345	81.1	180.1	0.44	17.4	5416	10.8
70	346	71.3	150.1	0.46	17.4	5268	5.6
71	347	72.1	150.9	0.46	16.2	5535	17.5
72	349	84.9	179.6	0.47	10.9	5860	51.5
73	350	64.8	154.4	0.41	10.6	4169	5.3
74	351	77.2	159.7	0.48	11.2	4825	15.0
75	354	69.8	163.2	0.42	9.7	5240	13.0
76	355	69.2	151.7	0.44	10.7	5732	13.7
77	356	81.3	171.7	0.46	19.8	5031	8.2
78	358	64.7	142.3	0.45	13.4	5700	8.0
79	360	85.3	167.6	0.50	17.8	5011	46.8

Appendix Table 5 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
80	361	90.0	173.9	0.51	14.6	4893	47.2
81	364	82.3	169.2	0.45	8.4	5479	11.0
82	365	64.8	143.7	0.44	20.9	4757	10.8
83	369	72.3	164.7	0.42	12.8	5106	32.7
84	370	79.3	162.4	0.48	20.7	5556	26.2
85	372	61.4	146.5	0.41	14.4	5351	8.8
86	373	82.1	170.1	0.48	13.0	5249	17.7
87	374	58.8	149.8	0.37	12.1	5256	1.7
88	377	86.3	175.9	0.48	18.0	5504	8.5
89	378	74.4	158.1	0.45	14.6	5744	50.9
90	380	78.5	158.2	0.48	13.0	6050	8.0
91	381	77.9	177.0	0.43	23.1	5278	28.5
92	382	84.1	170.6	0.49	13.4	5343	7.0
93	383	80.8	179.4	0.44	23.7	6133	3.8
94	384	65.9	161.6	0.40	13.8	4949	15.0
95	385	87.8	177.3	0.49	13.6	5286	62.0
96	388	83.9	175.3	0.47	9.6	5458	35.2
97	389	81.5	163.3	0.49	31.7	5769	67.8
98	390	65.0	148.6	0.43	13.5	4922	4.0
99	392	70.8	147.9	0.47	15.9	5416	28.5
100	396	75.5	156.6	0.47	26.1	5508	28.0
101	397	74.8	175.6	0.42	15.4	5690	31.9
102	400	70.4	167.0	0.42	17.3	6122	2.0
103	401	65.0	163.5	0.39	17.2	4439	3.0
104	402	74.8	174.3	0.42	18.9	5723	17.7
105	404	61.8	140.9	0.43	17.5	5034	9.8
106	408	80.0	171.1	0.47	20.6	5726	31.3

Appendix Table 5 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
107	409	87.3	183.1	0.47	13.9	4603	23.7
108	410	86.3	168.6	0.49	23.4	5304	20.0
109	411	95.4	197.2	0.48	21.7	4751	10.5
110	413	70.6	160.5	0.43	10.6	5329	3.5
111	414	79.1	169.0	0.46	12.4	5389	14.0
112	416	88.1	165.0	0.53	10.6	5366	24.0
113	417	86.5	171.2	0.49	29.2	5091	14.9
114	420	77.8	162.1	0.47	6.3	5530	12.2
115	423	74.4	151.1	0.48	19.7	5274	45.3
116	424	83.1	171.7	0.47	12.5	4910	17.5
117	427	78.6	167.8	0.46	11.6	5163	27.5
118	428	69.9	152.0	0.44	15.4	5755	12.3
119	430	67.9	160.7	0.41	17.9	5760	0.0
120	431	73.7	155.5	0.46	20.9	5679	10.0
121	432	68.4	158.8	0.42	10.7	5385	11.0
122	433	77.3	151.9	0.50	14.5	5059	18.3
123	435	71.1	169.1	0.42	11.1	5873	5.0
124	436	82.1	180.2	0.45	27.5	5141	23.8
125	437	73.9	141.1	0.51	8.9	5150	27.2
126	439	83.0	178.7	0.46	16.5	5028	20.3
127	440	80.1	157.3	0.50	20.2	4939	20.0
128	441	75.6	164.6	0.45	20.2	5533	15.2
129	443	80.6	166.4	0.47	24.7	5454	28.8
130	444	82.1	166.1	0.51	23.8	6696	10.8
131	445	82.4	170.6	0.48	23.9	5194	8.0
132	446	78.7	169.6	0.46	12.6	5404	33.0
133	447	69.3	150.0	0.46	18.2	5989	6.1

Appendix Table 5 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
134	449	61.0	132.8	0.46	14.0	5581	7.0
135	452	74.6	154.3	0.48	21.1	5322	33.3
136	454	86.8	167.1	0.52	10.3	5381	16.5
137	455	72.6	179.0	0.40	15.4	5266	19.2
138	459	90.2	162.9	0.54	13.8	5511	38.0
139	461	79.3	158.9	0.49	11.2	4926	36.8
140	462	81.8	177.5	0.46	16.7	5722	68.5
141	465	68.8	160.6	0.42	17.0	5277	6.8
142	466	82.1	175.6	0.47	7.5	5096	22.5
143	469	97.1	188.5	0.51	14.9	5701	72.7
144	470	101.9	201.8	0.50	17.8	4670	36.2
Average		76.8	162.9	0.46	16.2	5327	20.8
L.S.D. (.05)		10.4	15.7	0.05	6.3	793	22.0

Appendix Table 6. ERHT (ear height), PTHT (plant height), ERHT:PTHT (ear-height-to-plant-height ratio), TBN (tassel branch number), PLA (leaf area per plant) and LODG (percent lodged plants) for 144 S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
1	236	65.4	150.1	0.43	12.9	6943	3.1
2	237	78.3	168.9	0.46	21.6	6272	15.0
3	239	69.7	145.3	0.47	15.5	5526	13.4
4	242	85.7	180.2	0.47	13.2	5247	5.7
5	244	66.0	151.5	0.42	14.3	5399	10.6
6	245	80.9	161.6	0.49	10.3	5806	9.0
7	246	61.2	155.8	0.38	15.6	5610	6.1
8	247	56.3	139.7	0.39	13.3	4796	20.9
9	248	63.0	151.8	0.41	16.4	6077	5.9
10	249	82.8	166.8	0.49	16.1	6203	17.4
11	250	69.1	163.1	0.41	16.9	5288	8.1
12	253	72.3	171.4	0.41	15.6	6193	44.5
13	254	86.9	174.3	0.49	23.6	5928	23.5
14	255	69.8	149.5	0.46	12.0	5215	2.0
15	257	82.0	161.9	0.50	20.4	5356	20.5
16	258	63.2	148.0	0.42	14.1	5468	15.7
17	259	73.0	163.4	0.44	18.4	5334	20.1
18	260	77.4	173.7	0.44	17.4	5383	17.5
19	261	65.3	151.7	0.42	15.5	5181	7.7
20	262	68.6	155.8	0.43	17.2	5480	2.9
21	265	66.0	153.2	0.42	19.1	5589	7.5
22	266	64.3	142.2	0.45	15.2	5730	4.6
23	268	79.7	162.7	0.48	14.5	6100	24.5
24	270	72.1	157.0	0.45	10.2	5882	12.9
25	272	88.1	190.5	0.46	9.6	5868	30.8

[a]Measured in 1974 and 1975.

Appendix Table 6 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
26	274	69.9	159.0	0.44	22.1	5325	9.5
27	275	73.9	156.1	0.46	17.4	6017	29.3
28	276	66.9	161.5	0.41	15.4	5456	5.2
29	278	63.6	160.4	0.38	17.5	5570	18.1
30	281	71.6	152.2	0.46	11.0	5708	38.5
31	282	65.7	163.9	0.40	11.8	5615	20.3
32	283	58.7	154.8	0.37	8.3	5678	25.4
33	284	76.1	163.7	0.46	23.6	5543	2.8
34	285	77.7	173.9	0.45	20.8	5725	9.4
35	286	64.1	161.9	0.38	22.8	5073	2.3
36	287	69.8	166.7	0.40	11.0	5534	26.4
37	288	80.0	171.7	0.44	22.3	5976	9.8
38	289	81.4	159.7	0.50	23.0	5559	15.2
39	291	72.3	158.6	0.44	17.3	6365	19.0
40	292	74.6	161.2	0.46	15.3	5061	4.9
41	294	61.1	144.8	0.40	20.9	5903	-0.2
42	295	70.5	152.9	0.44	21.1	4715	10.0
43	298	59.4	134.6	0.45	14.2	5921	0.2
44	299	74.9	152.5	0.48	22.9	5409	51.9
45	300	82.3	179.4	0.46	19.5	5374	25.0
46	301	71.1	172.1	0.48	20.2	5882	0.3
47	302	65.5	161.1	0.39	14.0	5164	17.0
48	305	80.5	165.4	0.46	18.9	6337	13.4
49	306	69.0	146.6	0.47	19.3	5545	5.4
50	307	70.4	148.6	0.46	7.4	6093	7.1
51	310	72.1	156.3	0.45	21.3	5912	3.7
52	311	82.6	189.7	0.43	25.5	5509	21.1

Appendix Table 6 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
53	314	65.1	154.0	0.41	25.9	5577	13.7
54	315	63.3	148.4	0.41	14.4	5022	10.9
55	316	82.4	176.8	0.47	20.9	5039	16.6
56	318	66.2	141.9	0.46	16.4	5802	20.5
57	319	65.6	159.1	0.40	17.0	5133	3.7
58	320	74.7	170.5	0.43	11.9	5273	8.2
59	325	59.5	136.6	0.43	21.7	5415	21.4
60	326	54.5	136.1	0.38	23.2	5602	8.0
61	327	107.9	194.7	0.55	15.8	6015	33.2
62	328	81.8	187.2	0.43	20.9	5107	13.9
63	329	69.7	146.0	0.47	12.1	5935	17.4
64	330	70.2	169.2	0.41	15.0	5657	5.6
65	331	67.7	159.0	0.42	6.9	5506	6.2
66	336	79.1	152.4	0.52	14.6	6059	19.1
67	337	59.0	135.3	0.38	18.1	5380	0.9
68	343	75.3	154.9	0.48	18.9	5336	25.3
69	345	75.4	184.1	0.41	20.5	6074	11.2
70	346	61.5	147.1	0.41	17.2	5380	6.0
71	347	81.6	153.9	0.49	19.4	5806	15.9
72	349	81.1	179.2	0.45	11.7	5702	57.3
73	350	57.7	152.9	0.36	10.2	5522	4.7
74	351	69.8	152.9	0.44	12.1	5415	14.6
75	354	66.0	156.0	0.41	10.2	5921	9.5
76	355	66.0	156.4	0.41	13.2	5971	15.3
77	356	78.5	173.5	0.45	23.0	5549	7.2
78	358	60.2	140.4	0.42	11.5	5947	7.4
79	360	78.5	166.8	0.46	20.6	5047	26.2

Appendix Table 6 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
80	361	83.6	173.2	0.47	16.6	5190	30.3
81	364	80.7	164.8	0.49	9.7	5964	8.0
82	365	65.5	153.1	0.43	21.3	5035	2.8
83	369	67.4	164.6	0.40	14.6	5420	22.2
84	370	74.9	161.7	0.46	21.1	5591	22.6
85	372	63.9	150.8	0.41	16.5	6125	11.4
86	373	80.8	170.5	0.47	13.4	5607	8.4
87	374	54.4	140.2	0.37	9.0	5368	-1.8
88	377	77.9	171.1	0.44	21.0	5363	4.3
89	378	65.2	165.9	0.39	16.1	5974	31.5
90	380	75.4	158.5	0.46	14.1	6100	1.6
91	381	76.7	172.9	0.44	22.3	5915	19.4
92	382	75.0	161.6	0.47	15.1	5179	4.3
93	383	69.7	163.0	0.42	22.2	5525	1.7
94	384	68.5	166.7	0.40	14.4	5314	7.5
95	385	90.4	182.5	0.50	12.4	5612	50.5
96	388	81.1	176.8	0.45	9.9	5687	28.8
97	389	79.8	163.4	0.48	13.3	6160	15.8
98	390	62.2	145.4	0.42	15.5	5264	3.0
99	392	66.9	135.0	0.48	16.8	5605	18.1
100	396	70.1	148.9	0.46	27.3	5489	32.0
101	397	72.4	170.8	0.41	16.2	5724	24.6
102	400	64.5	161.4	0.38	16.7	6483	1.1
103	401	58.4	154.3	0.37	15.7	5037	3.8
104	402	63.9	165.1	0.37	20.5	5907	6.4
105	404	59.9	129.3	0.45	18.3	5279	6.1
106	408	79.4	175.0	0.44	18.2	5657	26.4

Appendix Table 6 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
107	409	84.0	178.3	0.46	14.5	5451	11.4
108	410	79.8	162.6	0.48	22.2	5503	16.5
109	411	90.4	197.4	0.45	22.2	6052	2.5
110	413	71.2	156.7	0.44	9.9	5404	2.0
111	414	82.4	176.0	0.46	14.2	5751	7.3
112	416	79.9	158.2	0.50	11.4	5668	15.2
113	417	82.4	176.5	0.46	29.8	5299	7.6
114	420	69.1	158.4	0.42	8.1	4905	5.2
115	423	68.5	149.6	0.47	20.8	5422	45.8
116	424	76.3	158.7	0.47	17.4	4825	5.9
117	427	78.7	173.1	0.45	12.2	4976	33.6
118	428	67.7	165.1	0.40	14.3	5565	8.1
119	430	66.6	163.9	0.39	17.6	5315	-0.2
120	431	72.8	157.2	0.45	20.4	5321	0.4
121	432	66.2	158.9	0.41	10.5	5063	4.7
122	433	71.9	144.4	0.49	15.4	5413	16.4
123	435	64.0	161.3	0.39	9.8	6193	-1.3
124	436	82.0	183.2	0.45	26.0	5444	17.1
125	437	79.3	143.0	0.54	10.6	5248	16.5
126	439	82.5	179.6	0.45	17.6	5394	15.4
127	440	76.1	159.3	0.48	13.6	5304	17.4
128	441	64.6	150.7	0.42	17.9	5647	10.5
129	443	69.8	154.8	0.45	24.2	5576	15.9
130	444	78.6	161.8	0.48	19.1	6533	8.2
131	445	74.7	159.1	0.46	27.2	5168	-0.8
132	446	72.2	166.6	0.42	12.1	6301	15.5
133	447	67.6	154.3	0.43	20.2	6216	6.9

Appendix Table 6 (Continued)

Entry	S_1 family	ERHT (cm)	PTHT (cm)	ERHT:PTHT	TBN	PLA[a] (cm^2)	LODG (%)
134	449	56.4	132.0	0.41	13.6	5100	-1.2
135	452	67.4	143.9	0.46	20.3	5986	11.9
136	454	80.9	174.1	0.46	7.4	5159	29.5
137	455	71.1	169.2	0.41	15.3	5361	27.9
138	459	89.1	163.3	0.53	15.1	5594	27.1
139	461	82.2	162.9	0.49	12.3	5120	25.3
140	462	76.2	175.8	0.42	14.9	5602	53.2
141	465	74.4	172.7	0.42	18.0	5516	4.7
142	466	84.4	178.4	0.47	8.1	4746	12.4
143	469	95.8	181.5	0.51	13.6	5680	63.6
144	470	89.0	182.8	0.46	16.9	5251	10.0
Average		72.7	161.1	0.44	16.5	5585	14.6
L.S.D. (.05)		10.9	14.8	0.006	4.0	852	24.6

Appendix Table 7. LOV_j, LOV_a, LOV_b (juvenile, above and below ear leaf orientation values, respectively), LOR_j and LOR_m (juvenile and mature canopy orientation ratings, respectively) for 144 random S_1 families from BSUL1 grown at two plant densities in 1975 and 1976

		96,875 pl/ha			42,383 pl/ha				
Entry	S_1 family	LOV_j[1]	LOV_a	LOV_b[1]	LOV_j[2]	LOV_a	LOV_b[2]	LOR_j[2]	LOR_m
1	236	59.7	53.0	51.3	52.4	55.2	56.6	1.0	2.5
2	237	62.7	55.9	59.4	63.8	55.7	56.8	2.5	2.5
3	239	59.3	49.4	45.4	50.2	44.4	44.5	1.5	2.0
4	242	56.9	57.7	54.1	48.4	48.7	48.9	1.1	2.0
5	244	53.4	57.1	50.9	53.9	49.5	45.7	1.0	2.5
6	245	61.0	41.5	36.5	45.7	40.7	34.9	1.3	1.5
7	246	64.5	60.6	53.7	53.0	59.3	53.7	1.5	2.0
8	247	51.4	36.4	38.0	54.3	35.5	44.4	1.6	1.2
9	248	59.6	61.1	52.3	54.5	60.0	55.4	1.5	2.0
10	249	57.8	48.9	46.9	49.1	57.2	51.6	1.9	2.8
11	250	57.5	54.9	51.3	45.4	58.2	48.1	1.1	2.0
12	253	50.3	35.0	31.9	45.9	36.7	42.3	1.0	1.3
13	254	58.2	60.6	50.4	52.9	62.0	56.7	1.5	3.1
14	255	62.4	54.4	54.4	62.0	51.9	52.4	1.2	2.0
15	257	54.9	50.9	47.6	50.9	45.9	50.6	1.4	2.0
16	258	57.6	45.2	40.8	50.2	47.1	44.7	1.3	1.5
17	259	58.9	53.8	48.1	57.2	55.1	55.4	1.8	2.0
18	260	49.9	58.0	47.7	51.1	51.8	51.3	1.0	2.8
19	261	58.0	41.4	35.1	49.9	46.8	45.2	1.8	1.8
20	262	52.8	34.4	35.1	51.4	32.7	40.4	1.0	1.0
21	265	51.7	45.0	44.7	46.2	45.3	44.1	1.5	1.8
22	266	64.6	59.1	61.4	59.8	61.0	59.8	2.3	2.1
23	268	55.4	48.6	42.4	48.1	54.4	48.3	1.1	2.0
24	270	53.9	47.0	41.8	47.8	41.4	40.9	1.0	1.9
25	272	57.1	49.0	51.8	52.5	46.8	50.4	1.4	1.7
26	274	53.3	45.1	43.6	44.5	44.3	44.9	1.2	1.4
27	275	53.8	49.2	51.6	43.3	47.4	48.2	1.3	1.9
28	276	59.0	41.4	43.0	52.0	39.4	37.2	1.8	1.6
29	278	60.2	51.1	44.1	49.5	53.8	47.1	1.6	2.0
30	281	59.5	59.7	58.2	58.6	60.1	59.0	2.0	3.2
31	282	65.2	47.9	49.2	56.4	55.0	53.2	2.0	2.5
32	283	58.7	38.2	48.1	50.5	41.9	49.0	1.0	1.7
33	284	63.9	62.2	52.6	53.0	60.7	59.7	2.5	2.5
34	285	58.5	57.0	56.7	54.8	59.4	53.1	1.8	3.0

[1]Measured in 1975 only.

[2]Measured in 1974 and 1975.

Appendix Table 7 (Continued)

Entry	S_1 family	96,875 pl/ha			42,383 pl/ha				
		LOV_j [1]	LOV_a	LOV_b [1]	LOV_j [2]	LOV_a	LOV_b [2]	LOR_j [2]	LOR_m
35	286	55.6	58.9	50.5	50.3	53.7	50.1	1.3	2.0
36	287	59.3	56.4	44.3	49.1	53.2	47.2	1.4	2.0
37	288	55.7	59.6	53.0	52.4	54.4	48.7	1.5	2.0
38	289	54.9	50.9	45.8	43.9	47.5	44.1	1.4	1.7
39	291	56.1	34.7	32.7	49.5	32.9	39.2	1.1	1.2
40	292	59.0	46.0	47.4	53.2	47.3	47.7	1.2	1.6
41	294	60.3	59.4	63.2	55.0	58.9	53.6	1.7	2.7
42	295	54.4	46.1	43.8	56.1	40.3	39.1	1.2	2.0
43	298	55.6	40.9	36.4	48.6	48.1	37.7	1.1	1.2
44	299	57.9	57.0	58.4	56.9	60.4	49.0	1.6	2.2
45	300	59.6	54.3	49.2	50.6	58.3	45.3	2.1	2.3
46	301	56.5	56.0	48.9	48.9	51.7	45.6	1.4	2.5
47	302	57.8	51.8	48.6	50.4	50.9	51.0	1.4	2.0
48	305	48.8	57.3	52.7	46.9	58.2	47.8	1.1	1.9
49	306	52.1	48.1	46.6	49.5	54.5	38.8	1.1	2.0
50	307	60.9	42.3	31.5	46.4	40.5	38.5	1.1	1.5
51	310	60.4	41.0	41.3	54.4	38.4	38.6	1.0	1.2
52	311	48.2	53.0	40.5	52.0	52.9	44.7	1.2	2.5
53	314	60.5	55.8	53.7	61.1	61.1	54.6	2.1	2.0
54	315	51.5	29.6	34.4	47.8	28.5	38.7	1.0	1.0
55	316	63.6	51.6	53.3	50.9	51.9	50.6	1.8	2.0
56	318	52.9	44.7	38.7	50.7	49.6	46.4	1.9	1.9
57	319	56.3	57.7	54.7	49.7	57.3	45.9	1.4	2.5
58	320	53.4	41.7	46.1	50.8	45.1	43.4	1.2	1.8
59	325	56.8	64.0	47.6	52.0	62.5	53.1	1.2	3.0
60	326	56.5	45.6	41.5	61.0	41.1	47.0	1.7	1.5
61	327	53.2	45.6	41.8	45.8	46.8	39.2	1.1	1.5
62	328	55.7	45.8	45.0	45.0	48.0	40.5	1.6	2.0
63	329	62.2	48.5	53.8	55.0	52.1	53.0	1.9	2.0
64	330	59.6	55.6	49.1	52.2	50.2	46.8	1.6	2.5
65	331	58.2	52.1	54.7	49.8	53.9	50.5	1.5	2.3
66	336	59.6	53.7	56.2	48.4	52.0	50.3	1.3	2.0
67	337	57.9	51.3	49.4	46.2	52.9	42.9	1.6	1.5
68	343	57.1	49.4	43.0	54.6	49.8	43.2	1.4	2.3
69	345	58.0	52.8	48.0	48.1	54.6	46.6	1.1	3.4
70	346	56.1	37.4	32.5	43.3	43.0	41.5	1.5	2.0
71	347	57.8	58.9	56.0	53.9	60.0	54.8	2.0	2.0
72	349	58.3	58.9	61.7	52.4	61.4	53.8	1.4	2.5
73	350	45.7	49.7	43.0	46.8	46.5	40.2	1.0	1.4
74	351	53.4	43.9	44.1	47.6	42.2	44.4	0.9	1.5
75	354	49.7	59.4	51.6	48.4	49.7	39.8	1.7	1.5

Appendix Table 7 (Continued)

Entry	S_1 family	96,875 pl/ha LOV_j[1]	LOV_a	LOV_b[1]	42,383 pl/ha LOV_j[2]	LOV_a	LOV_b[2]	LOR_j[2]	LOR_m
76	355	56.6	53.7	47.6	50.6	48.4	43.2	1.0	1.6
77	356	53.4	44.1	58.6	52.5	53.2	52.9	1.3	1.8
78	358	52.9	55.5	53.3	56.2	62.0	52.1	1.7	3.5
79	360	49.5	45.3	53.5	49.6	53.1	55.6	1.4	1.9
80	361	56.2	56.6	57.4	48.2	57.7	55.1	2.5	2.5
81	364	51.6	56.1	56.4	59.4	53.4	57.8	1.6	2.0
82	365	62.4	45.7	55.0	61.3	52.4	49.8	1.7	2.0
83	369	64.9	61.0	55.9	48.6	56.3	51.6	1.7	3.1
84	370	56.0	58.2	50.8	50.6	61.2	53.5	1.7	3.0
85	372	54.7	57.3	43.3	46.8	52.6	44.7	1.4	2.1
86	373	56.2	45.3	45.6	53.2	42.1	45.3	1.5	1.8
87	374	45.2	48.5	43.9	38.9	49.1	49.0	1.1	1.5
88	377	63.0	51.5	50.6	52.8	53.0	48.0	1.2	2.1
89	378	54.0	56.1	52.5	55.0	53.2	50.7	1.7	2.5
90	380	56.4	54.2	49.1	54.9	54.5	51.9	1.3	2.5
91	381	60.6	48.8	48.4	54.3	42.5	46.7	1.0	2.5
92	382	52.7	46.0	41.3	43.4	41.7	42.6	1.1	1.3
93	383	56.8	45.7	44.2	44.6	43.4	46.1	1.2	1.7
94	384	60.5	58.0	55.3	56.3	55.7	56.2	2.0	2.3
95	385	54.7	55.4	51.6	46.8	55.8	51.9	1.6	2.3
96	388	50.8	42.4	45.2	56.9	45.9	47.3	1.9	1.8
97	389	60.8	51.5	57.4	54.4	56.5	54.0	1.2	2.8
98	390	56.1	47.0	39.5	56.0	49.2	48.5	1.3	1.7
99	392	70.1	49.7	45.9	55.2	49.6	50.8	1.1	2.0
100	396	55.1	63.9	56.5	49.6	61.5	52.1	1.4	2.5
101	397	57.8	57.6	51.2	56.1	56.3	48.6	2.1	3.0
102	400	52.9	47.4	45.9	52.8	48.9	48.6	1.7	2.5
103	401	52.9	51.1	47.4	50.3	49.0	46.4	1.8	2.0
104	402	59.7	50.1	48.4	56.3	55.7	57.3	1.6	3.2
105	404	53.4	54.3	44.8	49.2	51.8	42.2	1.1	1.8
106	408	66.2	54.7	50.4	53.8	50.6	47.2	1.2	2.3
107	409	56.2	49.6	41.8	51.5	46.1	51.5	1.7	1.8
108	410	50.5	46.7	40.8	45.4	49.1	45.3	1.6	2.0
109	411	44.5	36.4	32.9	40.3	35.7	30.3	1.0	1.0
110	413	68.0	59.5	59.5	53.2	56.1	60.5	2.2	4.0
111	414	65.0	44.2	44.1	56.6	44.6	45.0	1.5	0.9
112	416	54.9	52.4	51.3	49.0	55.1	52.7	1.5	2.6
113	417	55.2	58.4	53.7	53.2	59.0	48.8	1.5	2.0
114	420	56.7	56.5	48.2	56.2	59.0	50.9	1.5	1.9
115	423	57.8	50.7	53.6	52.4	62.3	54.9	1.2	3.5
116	424	58.4	44.0	46.3	54.1	41.9	43.6	1.3	1.4

Appendix Table 7 (Continued)

Entry	S_1 family	96,875 pl/ha LOV_j[1]	LOV_a	LOV_b[1]	42,383 pl/ha LOV_j[2]	LOV_a	LOV_b[2]	LOR_j[2]	LOR_m
117	427	62.4	61.3	51.9	65.0	59.2	55.2	2.0	2.7
118	428	52.7	38.6	39.1	41.6	41.1	41.0	1.0	1.0
119	430	60.6	62.7	59.8	56.4	59.4	56.2	1.8	2.0
120	431	63.7	60.2	58.4	45.7	55.7	51.7	1.5	2.0
121	432	52.4	55.0	48.6	49.0	50.8	47.9	1.2	2.5
122	433	63.3	45.5	46.7	51.7	47.2	54.4	1.5	2.0
123	435	56.6	47.5	36.2	55.2	45.5	45.5	1.3	1.7
124	436	64.9	57.3	61.3	64.5	59.8	59.2	2.5	3.3
125	437	53.3	41.8	42.8	58.6	50.9	49.6	1.9	2.5
126	439	50.2	45.7	49.4	44.2	40.1	41.8	1.3	1.5
127	440	60.8	44.4	48.5	55.4	50.9	42.8	1.5	2.0
128	441	53.6	54.7	44.1	53.7	51.9	51.4	1.8	2.5
129	443	46.5	43.3	46.5	50.4	50.6	48.0	1.3	1.8
130	444	48.9	41.2	34.6	49.3	43.0	44.8	1.0	1.3
131	445	50.6	64.3	48.7	54.1	56.7	50.6	1.2	1.0
132	446	57.1	48.9	49.5	65.4	51.7	47.7	2.0	2.0
133	447	58.3	54.2	47.1	45.0	58.3	47.4	1.0	2.1
134	449	56.2	48.3	40.3	46.3	51.9	48.9	1.1	2.0
135	452	55.5	49.7	51.4	47.6	54.7	51.8	1.1	2.2
136	454	54.8	44.3	56.2	47.3	55.9	50.3	1.3	2.0
137	455	55.9	51.1	50.9	51.7	52.3	49.2	1.1	1.8
138	459	52.0	39.2	42.1	56.8	40.2	45.4	1.1	1.5
139	461	62.2	43.3	49.7	49.5	50.8	55.4	1.6	2.0
140	462	55.0	46.8	41.9	52.6	45.9	45.2	1.1	1.7
141	465	54.8	41.0	45.2	49.6	49.3	41.7	1.0	2.0
142	466	57.6	56.8	52.5	57.0	56.8	57.3	1.7	3.3
143	469	57.3	49.7	47.8	52.2	57.5	48.4	1.6	2.0
144	470	64.7	56.5	57.9	53.2	54.3	51.9	1.2	2.1
Average		56.7	50.6	48.1	51.6	50.9	48.3	1.5	2.1
L.S.D. (.05)		8.8	9.8	11.5	11.4	9.5	8.8	0.5	1.0

Appendix Table 8. CER (carbon dioxide exchange rate), SLW (specific leaf weight) and LT (leaf thickness) during grain filling of 64 random S_1 families from BSUL1 grown at 42,383 pl/ha in 1975 and 1976

Entry	S_1 family	CER (mg $CO_2/dm^2/hr$)	SLW (mg/cm^2)	LT (μ)
1	242	26.1	5.7	206
2	247	29.0	6.3	234
3	248	26.0	6.0	230
4	253	30.7	5.7	220
5	272	23.4	5.6	200
6	274	27.5	5.5	202
7	275	25.7	5.4	207
8	276	25.8	5.7	208
9	278	26.1	5.3	188
10	281	24.0	5.8	226
11	282	27.6	5.9	221
12	283	15.0	5.9	226
13	284	28.6	5.7	212
14	285	25.1	5.8	200
15	286	28.4	5.0	203
16	287	23.0	5.9	213
17	288	23.2	5.8	215
18	289	31.5	5.7	214
19	291	26.6	6.1	240
20	292	24.5	6.1	217
21	294	24.7	5.6	200
22	295	28.3	5.8	221
23	298	29.0	5.9	231
24	299	30.0	5.7	213
25	300	28.8	5.8	208
26	301	31.3	5.7	221
27	302	30.4	5.7	203
28	305	23.2	5.7	214
29	306	28.4	5.6	219
30	307	27.3	5.3	210
31	310	25.7	6.1	235
32	311	25.5	5.3	207
33	314	23.4	5.5	188
34	315	30.6	5.3	219
35	316	34.2	5.6	202
36	318	23.9	5.8	227
37	319	24.7	5.3	210
38	320	33.2	5.5	210

Appendix Table 8 (Continued)

Entry	S_1 family	CER (mg $CO_2/dm^2/hr$)	SLW (mg/cm^2)	LT (μ)
39	325	24.8	5.8	232
40	326	32.5	5.6	208
41	389	36.6	5.8	234
42	390	31.5	5.7	195
43	392	32.7	6.0	244
44	396	27.2	5.7	225
45	397	38.8	5.6	222
46	400	28.6	5.8	230
47	401	33.2	5.7	212
48	402	28.1	6.1	217
49	404	32.5	5.8	227
50	408	22.4	5.3	204
51	409	24.3	5.6	213
52	410	26.6	5.7	210
53	432	33.6	6.3	232
54	433	31.5	5.8	216
55	435	26.2	5.6	229
56	436	24.8	5.3	208
57	437	28.3	5.6	188
58	439	23.6	5.9	191
59	440	28.3	5.5	214
60	441	24.6	5.1	207
61	443	30.4	6.3	215
62	444	19.7	5.6	213
63	445	26.1	5.7	234
64	446	30.1	5.6	198
Mean		27.5	5.7	215
LSD (.05)		8.4	0.4	18

Appendix Table 9. Adjusted phenotypic correlations (above the diagonal) and genotypic correlations (below the diagonal) among all traits measured at 96,875 pl/ha in 1975 and 1976

Traits	YIELD	YIELDP	BARREN	PROLIF	GRNPLA[1]	STAND	PTHT	ERHT
YIELD		0.98**	-0.88**	0.88**	0.70**	0.10	0.01	0.10
YIELDP	0.96		-0.89**	0.89**	0.75**	-0.08	0.01	0.13
BARREN	-0.90	-0.90		-0.99**	-0.66**	0.05	0.12	-0.04
PROLIF	0.69	0.71	-0.82		0.66**	-0.05	-0.12	0.05
GRNPLA[1]	0.98	0.97	-0.97	0.95		-0.20*	0.03	0.15
STAND	0.14	0.06	-0.07	-0.04	0.06		0.03	-0.11
PTHT	-0.10	-0.11	0.23	-0.15	-0.25	0.19		0.78**
ERHT	0.13	0.15	0.02	0.10	-0.08	-0.20	0.79	
ERHT:PTHT	0.30	0.36	-0.29	0.32	-0.02	-0.63	0.12	0.69
TBN	-0.28	-0.29	0.28	-0.14	-0.42	0.05	0.19	0.17
PLA[1]	-0.14	0.01	0.49	-0.44	0.04	-0.31	0.15	-0.20
LODG	0.43	0.50	-0.35	0.42	0.15	-0.14	0.37	0.51
LOV_j[1]	0.11	0.12	-0.03	0.03	0.18	-0.15	-0.02	0.11
LOV_a	-0.08	-0.11	0.14	-0.12	-0.01	0.06	0.11	-0.01
LOV_b[1]	0.03	0.06	0.08	-0.07	0.06	-0.26	0.09	0.14
25%ANTH	-0.39	-0.37	0.47	-0.42	-0.57	-0.12	0.49	0.42
50%ANTH	-0.36	-0.34	0.46	-0.77	-0.56	-0.12	0.49	0.44
75%ANTH	-0.42	-0.39	0.51	-0.47	-0.53	-0.16	0.49	0.47
25%SILK	-0.63	-0.62	0.65	-0.55	-0.74	-0.03	0.41	0.25
50%SILK	-0.73	-0.74	0.80	-0.76	-0.80	0.08	0.36	0.22
75%SILK	-0.71	-0.72	0.77	-0.65	-0.92	0.08	0.30	0.14
PSS	-0.85	-0.89	0.87	-0.73	-0.76	0.26	0.17	0.05
SI	-0.85	-0.88	0.96	-0.83	-0.97	0.21	0.22	0.03
SD	-0.81	-0.85	0.81	-0.66	-0.84	0.22	0.10	-0.15

[1]Measured in 1975 only.

*,**Significant at the 5% and 1% levels of probability, respectively.

ERHT:PTHT	TBN	PLA[1]	LODG	LOV_j[1]	LOV_a	LOV_b[1]	25%ANTH
0.15	-0.23**	-0.18*	0.26**	0.15	-0.05	-0.01	-0.34**
0.20*	-0.22**	-0.16*	0.29**	0.16*	-0.05	0.01	-0.32**
-0.20*	0.22**	0.22**	-0.29**	-0.11	0.10	0.10	0.41**
0.20*	-0.22**	-0.22**	0.29**	0.11	-0.09	-0.07	-0.41**
0.22**	-0.20*	-0.08	0.35**	0.11	0.00	0.04	-0.20*
0.22**	0.00	-0.04	-0.14	-0.04	-0.10	-0.08	-0.01
0.10	0.17*	0.00	0.29**	-0.04	0.06	0.11	0.41**
0.69**	0.18*	0.03	0.43**	-0.01	0.00	0.12	0.37**
	0.10	0.09	0.36**	0.05	-0.07	0.07	0.14
0.08		0.10	0.04	-0.01	0.13	0.11	0.18*
-0.51	-0.18		0.06	-0.07	0.03	-0.03	0.32**
0.44	-0.09	0.49		0.07	0.02	0.15	0.08
0.32	-0.09	-0.65	0.17		0.30**	0.41**	-0.12
-0.15	0.16	0.06	0.05	0.48		0.73**	0.19*
0.19	0.16	-0.22	0.19	0.75	0.94		0.22**
0.16	0.18	0.57	0.10	-0.14	0.24	0.27	
0.17	0.21	0.46	0.13	-0.18	0.25	0.22	0.99
0.26	0.24	0.52	0.16	-0.23	0.25	0.18	0.97
-0.06	0.38	0.14	-0.16	-0.14	0.30	0.25	0.83
-0.05	0.43	0.26	-0.23	-0.18	0.25	0.14	0.79
-0.11	0.32	0.37	-0.23	-0.21	0.20	0.13	0.60
-0.25	0.48	0.04	-0.48	-0.13	0.18	0.03	0.43
-0.19	0.29	0.56	-0.33	-0.27	0.10	-0.02	0.37
-0.36	0.38	0.03	-0.53	-0.19	0.16	0.03	0.33

Appendix Table 9 (Continued)

Traits	50%ANTH	75%ANTH	25%SILK	50%SILK	75%SILK	PSS	SI	SD
YIELD	-0.34**	-0.33**	-0.58**	-0.66**	-0.73**	-0.70**	-0.69**	-0.71**
YIELDP	-0.33**	-0.32**	-0.57**	-0.66**	-0.74**	-0.72**	-0.70**	-0.73**
BARREN	0.43**	0.42**	0.61**	0.73**	0.80**	0.74**	0.79**	0.73**
PROLIF	-0.42**	-0.41**	-0.60**	-0.72**	-0.80**	-0.74**	-0.79**	-0.73**
GRNPLA[1]	-0.21**	-0.20**	-0.47**	-0.56**	-0.58**	-0.65**	-0.54**	0.64**
STAND	0.00	-0.05	0.01	0.04	0.06	0.06	0.09	0.10
PTHT	0.41**	0.40**	0.31**	0.27**	0.24	0.08	0.11	0.01
ERHT	0.37**	0.40**	0.19*	0.16*	0.08	-0.06	-0.04	-0.17*
ERHT:PTHT	0.15	0.20*	-0.04	-0.05	-0.13	-0.20**	-0.19*	-0.28**
TBN	0.20*	0.21**	0.34**	0.35**	0.30**	0.35**	0.21**	0.27**
PLA[1]	0.35**	0.36**	0.25**	0.29**	0.26**	0.14	0.21**	0.10
LODG	0.08	0.11	-0.14	-0.21**	-0.24**	-0.37**	-0.28**	-0.43**
LOV_j[1]	-0.13	-0.12	-0.11	-0.14	-0.15	-0.11	0.14	-0.09
LOV_a	0.18*	0.18*	0.22**	0.20*	0.16*	0.15	0.06	0.11
LOV_b[1]	0.20**	0.22**	0.22**	0.18*	0.14	0.12	0.03	0.04
25%ANTH	0.98**	0.94**	0.80**	0.74**	0.64**	0.34**	0.31**	0.26**
50%ANTH		0.97**	0.80**	0.76**	0.67**	0.35**	0.35**	0.27**
75%ANTH	0.97		0.77**	0.75**	0.65**	0.35**	0.36**	0.24**
25%SILK	0.84	0.81		0.92**	0.85**	0.73**	0.48**	0.67**
50%SILK	0.80	0.84	0.97		0.93**	0.87**	0.67**	0.76**
75%SILK	0.62	0.63	0.80	0.86		0.85**	0.86**	0.84**
PSS	0.45	0.45	0.81	0.88	0.83		0.73**	0.89**
SI	0.40	0.46	0.63	0.79	0.78	0.92		0.77**
SD	0.34	0.34	0.74	0.81	0.79	0.98	0.90	

Appendix Table 10. Adjusted phenotypic correlations (above the diagonal) and genotypic correlations (below the diagonal) among all traits measured at 42,383 pl/ha in 1975 and 1976

Traits	YIELD	YIELDP	BARREN	PROLIF	SECOND	GRNPLA[1]	STAND
YIELD		0.97**	-0.71**	0.73**	0.38**	0.68**	0.23**
YIELDP	1.00		-0.73**	0.74**	0.38**	0.65**	0.06
BARREN	-0.87	-0.88		-0.87**	-0.24**	-0.50**	-0.11
PROLIF	0.87	0.84	0.95		0.63**	0.51**	0.10
SECOND	0.62	0.53	-0.48	0.71		0.26**	0.03
GRNPLA[1]	0.93	0.94	-0.88	0.71	0.41		0.10
STAND	0.68	0.80	-1.00	0.98	0.58	-0.06	
PTHT	0.14	0.17	-0.02	0.05	0.14	0.19	-0.59
ERHT	0.27	0.31	-0.18	0.28	0.44	0.21	-1.30
ERHT:PTHT	0.27	0.29	-0.26	0.42	0.56	0.18	-1.24
TBN	-0.18	-0.14	0.14	-0.14	-0.11	-0.10	-0.05
PLA[1]	-0.10	-0.17	0.36	-0.34	-0.22	-0.40	1.19
LODG	0.50	0.55	-0.32	0.47	0.46	-0.09	0.16
LOV_j[1]	0.20	0.20	-0.19	0.16	0.14	0.32	-0.44
LOV_a	-0.17	-0.19	0.29	-0.18	0.04	0.07	-0.07
LOV_b	0.14	0.14	-0.10	0.10	0.09	0.20	-1.15
LOR_j[1]	0.10	0.15	-0.16	0.06	0.00	0.23	-1.31
LOR_m	0.30	0.28	-0.24	0.24	0.04	0.29	0.47
25%ANTH	-0.17	-0.20	0.24	-0.14	0.06	-0.48	-0.60
50%ANTH	-0.20	-0.20	0.26	-0.19	-0.05	-0.51	-0.98
75%ANTH	-0.28	-0.27	0.32	-0.26	-0.10	-0.51	-1.21
25%SILK	-0.42	-0.43	0.51	-0.45	-0.22	-0.63	-0.70
50%SILK	-0.50	-0.51	0.55	-0.54	-0.34	-0.65	-0.88
75%SILK	-0.65	-0.68	0.75	-0.72	-0.42	-0.64	-0.80
PSS	-0.72	-0.73	0.71	-0.81	-0.59	-0.44	-1.41
SI	-0.80	-0.86	0.87	-0.90	-0.60	-0.42	-0.59
SD	-0.76	-0.79	0.85	-0.88	-0.60	-0.55	-0.41

[1]Measured in 1975 only.

*,**Significant at the 5% and 1% levels of probability, respectively.

PTHT	ERHT	ERHT:PTHT	TBN	PLA[1]	LODG	LOV_j[1]
0.19*	0.24**	0.18*	-0.16*	0.02	0.16*	0.03
0.20**	0.26**	0.20*	-0.14	-0.02	0.15	0.06
-0.04	-0.13	-0.18*	0.11	0.10	-0.15	0.00
0.07	0.20**	0.25**	-0.11	-0.06	0.19*	0.03
0.11	0.27**	0.29**	-0.07	0.05	0.17*	0.01
0.21**	0.35**	0.34**	-0.06	-0.08	0.22**	0.00
-0.07	-0.13	-0.15	-0.09	0.06	0.05	0.03
	0.77**	0.18*	0.09	0.04	0.30**	-0.02
0.81		0.75**	0.09	0.06	0.41**	-0.01
0.23	0.78		0.06	0.05	0.34**	0.03
0.11	0.08	0.05		-0.04	-0.07	0.02
0.06	0.01	-0.08	-0.16		0.04	-0.04
0.48	0.64	0.54	-0.11	-0.08		0.07
0.04	0.17	0.29	0.11	-0.35	0.20	
0.02	0.05	0.05	0.18	-0.29	0.19	0.58
0.15	0.14	0.07	0.04	-0.26	0.27	0.69
0.13	0.11	0.04	0.16	-0.43	0.11	0.63
0.15	0.04	0.03	0.11	-0.16	0.34	0.66
0.42	0.40	0.27	0.14	0.38	0.15	-0.18
0.41	0.40	0.27	0.15	0.42	0.17	-0.11
0.40	0.38	0.24	0.19	0.39	0.15	-0.11
0.33	0.27	0.10	0.32	0.31	-0.01	-0.21
0.34	0.28	0.10	0.35	0.33	-0.04	-0.23
0.28	0.19	0.02	0.32	0.34	-0.11	-0.34
0.11	0.00	-0.17	0.50	0.00	-0.32	-0.29
0.06	-0.08	-0.17	0.21	0.27	-0.23	-0.53
0.03	-0.13	-0.27	0.39	0.05	-0.35	-0.38

Appendix Table 10 (Continued)

Traits	LOV_a	LOV_b[1]	LOR_j[1]	LOR_m	25%ANTH	50%ANTH
YIELD	-0.04	0.01	0.06	0.19*	-0.19*	-0.20*
YIELDP	-0.05	0.01	0.10	0.17*	-0.18*	-0.19*
BARREN	0.10	0.10	-0.07	-0.07	0.18*	0.20*
PROLIF	-0.06	-0.09	0.06	0.09	-0.11	-0.15
SECOND	0.04	0.00	0.01	0.06	0.04	-0.01
GRNPLA[1]	-0.06	0.00	0.05	0.03	-0.11	-0.11
STAND	-0.04	0.01	-0.12	0.07	-0.12	-0.14
PTHT	0.03	0.01	0.07	0.10	0.36**	0.36**
ERHT	0.05	0.04	0.06	0.05	0.35**	0.35**
ERHT:PTHT	0.06	0.08	0.02	0.02	0.21**	0.22**
TBN	0.18*	0.03	0.06	0.06	0.14	0.15
PLA[1]	0.02	-0.02	-0.09	0.06	0.25**	0.27**
LODG	0.16*	0.15	0.09	0.18*	0.12	0.10
LOV_j[1]	0.31**	0.49**	0.50**	0.33**	-0.11	-0.11
LOV_a		0.73**	0.45**	0.69**	0.19*	0.19*
LOV_b	0.97		0.53**	0.64**	0.13	0.14
LOR_j[1]	0.70	0.73		0.42**	-0.02	0.00
LOR_m	0.93	0.87	0.63		0.17*	0.17*
25%ANTH	0.24	0.09	-0.05	0.20		0.96**
50%ANTH	0.23	0.12	-0.04	0.22	1.00	
75%ANTH	0.23	0.12	-0.04	0.18	0.99	1.01
25%SILK	0.22	0.08	-0.01	0.14	0.91	0.92
50%SILK	0.24	0.02	-0.01	0.17	0.88	0.90
75%SILK	0.25	-0.04	-0.04	0.03	0.79	0.81
PSS	0.16	-0.14	0.06	0.03	0.33	0.39
SI	0.22	-0.33	-0.09	0.10	0.24	0.25
SD	0.16	-0.10	0.01	-0.09	0.25	0.27

75%ANTH	25%SILK	50%SILK	75%SILK	PSS	SI	SD
-0.24**	-0.34**	-0.39**	-0.49**	-0.44**	-0.51**	-0.55**
-0.22**	-0.34**	-0.38**	-0.50**	-0.44**	-0.51**	-0.56**
0.22**	0.35**	0.41**	0.55**	0.48**	0.62**	0.61**
-0.19*	-0.32**	-0.39**	-0.53**	-0.49**	-0.61**	-0.63**
-0.05	-0.13	-0.18*	-0.21**	-0.26**	-0.26**	-0.34**
-0.15	-0.24**	-0.28**	-0.35**	-0.35**	-0.38**	-0.46**
-0.21**	-0.08	-0.10	-0.09	-0.01	-0.08	-0.01
0.35**	0.28**	0.29**	0.23**	0.08	0.04	0.01
0.33**	0.21**	0.20**	0.12	-0.06	-0.07	-0.15
0.21**	0.06	0.05	-0.02	-0.17*	-0.15	-0.25**
0.19*	0.29**	0.32**	0.27**	0.40**	0.16	0.33**
0.25**	0.27**	0.25**	0.23**	0.11	0.06	0.12
0.07	-0.01	-0.04	-0.11	-0.21**	-0.19*	-0.26**
-0.12	-0.13	-0.10	-0.10	-0.04	-0.01	-0.06
0.18	0.18*	0.20*	0.18	0.13	0.10	0.11
0.13	0.09	0.11	0.10	0.03	0.07	0.03
0.03	-0.02	0.01	-0.05	0.02	-0.06	-0.04
0.15	0.10	0.12	0.05	0.02	-0.02	-0.03
0.92**	0.84**	0.80**	0.71**	0.24**	0.18*	0.21**
0.96**	0.86**	0.84**	0.74**	0.27**	0.22**	0.24**
	0.85**	0.83**	0.74**	0.31**	0.25**	0.26**
0.94		0.97**	0.88**	0.66**	0.31**	0.61**
0.92	1.01		0.91**	0.74**	0.42**	0.67**
0.84	0.94	0.94		0.70**	0.71**	0.77**
0.42	0.73	0.75	0.76		0.47**	0.90**
0.29	0.41	0.45	0.70	0.56		0.67**
0.32	0.63	0.67	0.77	1.00	0.73	

Appendix Table 11. Adjusted phenotypic correlations between traits of BSUL1 measured at two densities

	96,875 pl/ha				
42,383 pl/ha	YIELD	YIELDP	BARREN	PROLIF	GRNPLA
YIELD	0.75**	0.74**	-0.62**	0.62**	0.46**
YIELDP	0.74**	0.74**	-0.63**	0.62**	0.46**
BARREN	-0.59**	-0.59**	0.66**	-0.66**	-0.39**
PROLIF	0.63**	0.64**	-0.68**	0.68**	0.44**
SECOND	0.40**	0.38**	-0.31**	0.32**	0.29**
GRNPLA	0.53**	0.54**	-0.44**	0.44**	0.54**
STAND	0.08	0.03	-0.04	0.05	0.00
PTHT	-0.01	-0.01	0.10	-0.10	0.06
ERHT	0.10	0.12	-0.04	0.05	0.18
ERHT:PTHT	0.14	0.18*	-0.16	0.16*	0.20*
TBN	-0.26**	-0.26**	0.22**	-0.23**	-0.22**
PLA	-0.11	-0.12	0.14	-0.14	-0.09
LODG	0.15	0.17*	-0.19*	0.20*	0.25**
LOV_j	0.02	0.16*	-0.03	0.03	0.04
LOV_a	-0.05	-0.05	0.08	-0.07	0.01
LOV_b	-0.01	0.01	0.08	-0.08	0.09
LOR_j	0.09	0.09	-0.11	0.11	0.09
LOR_m	0.15	0.13	-0.08	0.09	0.11
25%ANTH	-0.31**	-0.31**	0.39**	-0.39**	-0.17*
50%ANTH	-0.34**	-0.33**	0.41**	-0.41**	-0.20*
75%ANTH	-0.35**	-0.34**	0.42**	-0.42**	-0.22**
25%SILK	-0.48**	-0.48**	0.53**	-0.53**	-0.37**
50%SILK	-0.51**	-0.51**	0.56**	-0.56**	-0.39**
75%SILK	-0.59**	-0.59**	0.66**	-0.66**	-0.40**
PSS	-0.48**	-0.51**	0.49**	-0.49**	-0.45**
SI	-0.49**	-0.48**	0.55**	-0.55**	-0.27**
SD	-0.58**	-0.60**	0.60**	-0.60**	-0.49**

*,**Significant at the 5% and 1% level of probability, respectively.

96,875 pl/ha						
STAND	PTHT	ERHT	ERHT:PTHT	TBN	PLA	LODG
0.04	0.14	0.22**	0.21**	-0.09	-0.10	0.29**
0.00	0.16*	0.24**	0.21**	-0.08	-0.11	0.28**
-0.02	0.02	-0.07	-0.15	0.11	0.16	-0.27**
0.02	0.01	0.13	0.21**	-0.07	-0.16	0.33**
0.00	0.12	0.26**	0.27**	0.02	-0.10	0.29**
0.01	0.13	0.29**	0.33**	-0.05	-0.05	0.25**
0.27**	-0.13	-0.14	-0.07	-0.03	-0.01	0.00
0.01	0.89**	0.72**	0.13	0.08	0.00	0.33**
-0.07	0.70**	0.89**	0.62**	0.10	0.01	0.47**
-0.13	0.18*	0.64**	0.82**	0.08	0.03	0.39**
-0.03	0.15	0.16*	0.06	0.88**	0.02	-0.05
0.03	0.03	0.05	0.06	0.03	0.58**	0.06
-0.05	0.25**	0.36**	0.30**	-0.04	0.10	0.80**
-0.13	-0.05	-0.05	-0.01	0.01	-0.02	0.13
-0.07	0.01	0.04	0.04	0.15	0.06	0.12
-0.17*	0.00	0.05	0.08	0.04	0.05	0.15
-0.01	0.03	0.03	0.01	0.03	-0.12	0.08
0.02	0.04	0.02	0.01	0.08	0.08	0.15
0.04	0.35**	0.32**	0.14	0.16	0.34**	0.10
0.00	0.33**	0.33**	0.17*	0.17*	0.36**	0.09
-0.04	0.36**	0.34**	0.15	0.21**	0.32**	0.06
0.07	0.27**	0.21**	0.03	0.27**	0.32**	-0.06
0.03	0.29**	0.20**	0.01	0.30**	0.29**	-0.08
0.02	0.27**	0.16	-0.05	0.27**	0.29**	-0.16*
0.07	0.10	-0.03	-0.18*	0.33**	0.06	-0.25**
-0.06	0.13	0.00	-0.14	0.14	0.14	-0.23**
0.08	0.06	-0.09	-0.23**	0.26**	0.21**	-0.33**

Appendix Table 11 (Continued)

42,383 pl/ha	96,875 pl/ha				
	LOV_j	LOV_a	LOV_b	25%ANTH	50%ANTH
YIELD	0.14	-0.04	0.08	-0.18*	-0.18*
YIELDP	0.15	-0.04	0.08	-0.18*	-0.17*
BARREN	-0.11	0.15	0.01	0.20*	0.21**
PROLIF	0.14	-0.10	0.03	-0.13	-0.14
SECOND	0.11	0.02	0.07	0.05	0.06
GRNPLA	0.05	-0.09	0.04	-0.09	-0.10
STAND	0.01	-0.04	0.05	-0.04	-0.15
PTHT	-0.03	0.06	0.14	0.42**	0.41**
ERHT	0.00	0.02	0.14	0.39**	0.39**
ERHT:PTHT	0.05	-0.05	0.08	0.23**	0.23**
TBN	-0.03	0.19*	0.11	0.16*	0.17*
PLA	-0.05	0.00	-0.07	0.23**	0.26**
LODG	0.00	0.03	0.12	0.08	0.10
LOV_j	0.43**	0.28**	0.39**	-0.02	-0.02
LOV_a	0.32**	0.83**	0.75**	0.20*	0.19*
LOV_b	0.43**	0.63**	0.73**	0.15	0.13
LOR_j	0.38**	0.37**	0.44**	-0.02	-0.03
LOR_m	0.34**	0.60**	0.57**	0.17*	0.16*
25%ANTH	-0.11	0.15	0.19*	0.94**	0.93**
50%ANTH	-0.11	0.14	0.20*	0.93**	0.93**
75%ANTH	-0.12	0.16*	0.19*	0.90**	0.91**
25%SILK	-0.13	0.16*	0.16*	0.80**	0.82**
50%SILK	-0.10	0.19*	0.20*	0.76**	0.78**
75%SILK	-0.10	0.19*	0.16*	0.69**	0.71**
PSS	-0.04	0.17*	0.12	0.21**	0.24**
SI	-0.01	0.18*	0.10	0.21**	0.23**
SD	-0.06	0.18*	0.09	0.19*	0.21**

96,875 pl/ha						
75%ANTH	25%SILK	50%SILK	75%SILK	PSS	SI	SD
-0.18*	-0.38**	-0.47**	-0.53**	-0.55**	-0.53**	-0.57**
-0.17*	-0.38**	-0.46**	-0.53**	-0.54**	-0.54**	-0.57**
0.22**	0.40**	0.51**	0.58**	0.60**	0.60**	0.61**
-0.15	-0.37**	-0.47**	-0.55**	-0.59**	-0.59**	-0.62**
0.04	-0.15	-0.20*	-0.23**	-0.34**	-0.24**	-0.33**
-0.10	-0.29**	-0.33**	-0.44**	-0.42**	-0.47**	-0.49**
-0.14	-0.08	-0.10	-0.02	-0.04	-0.04	0.05
0.40**	0.32**	0.27*	0.22**	0.07	0.07	0.01
0.38**	0.20*	0.15	0.07	-0.08	-0.06	-0.18*
0.23**	0.01	-0.01	-0.09	-0.19*	-0.17*	-0.28**
0.17*	0.36**	0.37**	0.32**	0.39**	0.22**	0.33**
0.25**	0.22**	0.20**	0.22**	0.10	0.18*	0.14
0.14	-0.07	-0.12	0.16*	-0.24**	-0.20**	-0.30**
0.01	-0.05	-0.07	-0.12	-0.09	-0.14	-0.13
0.21**	0.22**	0.20*	0.17	0.15	0.08	0.11
0.17*	0.10	0.08	0.05	0.02	0.00	-0.04
0.00	-0.01	-0.06	-0.13	-0.07	-0.20*	-0.08
0.19*	0.12	0.05	0.02	-0.04	-0.08	-0.06
0.90**	0.77**	0.72**	0.62**	0.35**	0.31**	0.26**
0.92**	0.78**	0.76**	0.66**	0.39**	0.35**	0.29**
0.91**	0.78**	0.76**	0.66**	0.41**	0.35**	0.29**
0.79**	0.91**	0.89**	0.81**	0.66**	0.48**	0.59**
0.77**	0.91**	0.89**	0.83**	0.70**	0.51**	0.63**
0.69**	0.85**	0.89**	0.88**	0.76**	0.65**	0.70**
0.24**	0.65**	0.66**	0.67**	0.77**	0.50**	0.76**
0.23**	0.39**	0.51**	0.59**	0.57**	0.62**	0.55**
0.19**	0.63**	0.68**	0.73**	0.82**	0.62**	0.84**